```
OS   Herpes simplex virus (type 2).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Alphaherpesvirinae; Simplexvirus.
OX   NCBI_TaxID=10310;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HG52;
RX   MEDLINE=87111457; PubMed=3027242;
RA   McGeoch D.J., Moss H.W., McNab D., Frame M.C.;
RT   "DNA sequence and genetic content of the HindIII l region in the short
RT   unique component of the herpes simplex virus type 2 genome:
RT   identification of the gene encoding glycoprotein G, and evolutionary
RT   comparisons.";
RL   J. Gen. Virol. 68:19-38(1987).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HG52;
RX   MEDLINE=90278430; PubMed=2161906;
RA   Everett R., Fenwick M.;
RT   "Comparative DNA sequence analysis of the host shutoff genes of
RT   different strains of herpes simplex virus: type 2 strain HG52 encodes
RT   a truncated UL41 product.";
RL   J. Gen. Virol. 71:1387-1390(1990).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HG52;
RX   MEDLINE=92113549; PubMed=1662697;
RA   McGeoch D.J., Cunningham C., McIntyre G., Dolan A.;
RT   "Comparative sequence analysis of the long repeat regions and
RT   adjoining parts of the long unique regions in the genomes of herpes
RT   simplex viruses types 1 and 2.";
RL   J. Gen. Virol. 72:3057-3075(1991).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HG52;
RX   MEDLINE=92356101; PubMed=1322965;
RA   Barnett B.C., Dolan A., Telford E.A.R., Davison A.J., McGeoch D.J.;
RT   "A novel herpes simplex virus gene (UL49A) encodes a putative membrane
RT   protein with counterparts in other herpesviruses.";
RL   J. Gen. Virol. 73:2167-2171(1992).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HG52;
RA   Dolan A.;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z86099; CAB06753.1; -.
DR   InterPro; IPR000501; Proc_transport.
DR   Pfam; PF01366; PRTP; 1.
SQ   SEQUENCE   785 AA;  85240 MW;  246988E41997DF62 CRC64;

  Query Match             36.4%;  Score 44;  DB 12;  Length 785;
  Best Local Similarity   41.7%;  Pred. No. 15;
  Matches   10;  Conservative    4;  Mismatches   10;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLKNGGXSSGA 35
              :| :|||:|     |  || : ||
Db        422 EQCDEEALRRVLARLGAGGATGGA 445


RESULT 3
Q9CIF8
ID   Q9CIF8      PRELIMINARY;      PRT;   310 AA.
AC   Q9CIF8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Mevalonate kinase.
GN   YEAG OR LL0404.
OS   Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC   Streptococcaceae; Lactococcus.
OX   NCBI_TaxID=1360;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IL1403;
RX   MEDLINE=21235186; PubMed=11337471;
RA   Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
RA   Weissenbach J., Ehrlich S.D., Sorokin A.;
RT   "The complete genome sequence of the lactic acid bacterium Lactococcus
RT   lactis ssp. lactis IL1403.";
RL   Genome Res. 11:731-753(2001).
DR   EMBL; AE006277; AAK04502.1; -.
DR   InterPro; IPR001745; GHMPknse_ATP.
DR   InterPro; IPR001459; Mev_gal_kin.
DR   Pfam; PF00288; GHMP_kinases; 1.
DR   PRINTS; PR00959; MEVGALKINASE.
KW   Kinase; Complete proteome.
SQ   SEQUENCE   310 AA;  34334 MW;  E85A2C962C943BDA CRC64;

  Query Match             34.7%;  Score 42;  DB 16;  Length 310;
  Best Local Similarity   33.3%;  Pred. No. 13;
  Matches    7;  Conservative    7;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         13 QXEEEAVRLXXXXLKNGGXSS 33
              : |::|:|:    ||||  ::
Db        285 ENEKDAIRISQRLLKNGAKNT 305


RESULT 4
Q8ZQW9
ID   Q8ZQW9      PRELIMINARY;      PRT;   546 AA.
AC   Q8ZQW9;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Phosphoglucomutase (EC 5.4.2.2).
GN   PGM OR STM0698.
OS   Salmonella typhimurium.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Salmonella.
OX   NCBI_TaxID=602;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX   MEDLINE=21534948; PubMed=11677609;
RA   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA   Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA   Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA   Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA   Waterston R., Wilson R.K.;
RT   "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT   LT2.";
RL   Nature 413:852-856(2001).
DR   EMBL; AE008728; AAL19642.1; -.
DR   InterPro; IPR001485; PG/PMM_mutase.
DR   Pfam; PF00408; PGM_PMM; 1.
DR   Pfam; PF02878; PGM_PMM_I; 1.
DR   Pfam; PF02879; PGM_PMM_II; 1.
DR   Pfam; PF02880; PGM_PMM_III; 1.
DR   TIGRFAMs; TIGR01132; pgm; 1.
DR   PROSITE; PS00710; PGM_PMM; 1.
KW   Isomerase; Complete proteome.
SQ   SEQUENCE   546 AA;  58089 MW;  A3DD0779F6AE8C95 CRC64;

  Query Match             34.7%;  Score 42;  DB 16;  Length 546;
  Best Local Similarity   52.9%;  Pred. No. 24;
  Matches    9;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLKN 28
              || |:||| :    |||
Db        529 KQIEKEAVEIVSEVLKN 545


RESULT 5
Q8Z8F1
ID   Q8Z8F1      PRELIMINARY;      PRT;   546 AA.
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 24, 2003, 23:02:15 ; Search time 49.5 Seconds
(without alignments)
166.503 Million cell updates/sec

Title: US-09-889-331A-47
Perfect score: 121
Sequence: 1 XXXGTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGAXXXXX 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	44	36.4	234	5	Q9NM02	Q9nm02 leishmania
2	44	36.4	785	12	P89451	P89451 herpes simp
3	42	34.7	310	16	Q9CIF8	Q9cif8 lactococcus
4	42	34.7	546	16	Q8ZQW9	Q8zqw9 salmonella
5	42	34.7	546	16	Q8Z8F1	Q8z8f1 salmonella
6	42	34.7	546	16	Q8X9G6	Q8x9g6 escherichia
7	41	33.9	157	16	Q9RRJ0	Q9rrj0 deinococcus
8	41	33.9	167	16	Q9ADJ9	Q9adj9 streptomyce
9	41	33.9	266	13	O42143	O42143 xenopus lae
10	41	33.9	306	12	O92527	O92527 carnation l
11	41	33.9	402	17	Q9UYT6	Q9uyt6 pyrococcus
12	41	33.9	589	4	Q96L69	Q96169 homo sapien
13	41	33.9	2044	5	Q9VRN8	Q9vrn8 drosophila
14	41	33.9	2045	5	Q9VRN7	Q9vrn7 drosophila
15	40	33.1	127	16	P96631	P96631 bacillus su
16	40	33.1	374	5	Q9U184	Q9u184 leishmania
17	40	33.1	455	10	Q9LHL3	Q9lhl3 arabidopsis
18	40	33.1	567	5	Q9GNX7	Q9gnx7 leishmania
19	40	33.1	609	10	Q9SD72	Q9sd72 arabidopsis
20	40	33.1	731	5	Q9VZK7	Q9vzk7 drosophila
21	40	33.1	772	10	Q9SN69	Q9sn69 arabidopsis
22	40	33.1	773	5	Q8T919	Q8t919 drosophila
23	40	33.1	1296	2	Q9KGX3	Q9kgx3 mycoplasma
24	40	33.1	2382	5	Q9NKP4	Q9nkp4 leishmania
25	39	32.2	145	2	P70746	P70746 aeromonas h
26	39	32.2	208	17	O58594	O58594 pyrococcus
27	39	32.2	342	2	Q9Z3U2	Q9z3u2 pseudomonas
28	39	32.2	342	2	Q9R733	Q9r733 pseudomonas
29	39	32.2	342	2	Q9R2T7	Q9r2t7 pseudomonas
30	39	32.2	343	2	O31180	O31180 pseudomonas
31	39	32.2	580	16	Q988F6	Q988f6 rhizobium l
32	39	32.2	644	10	Q8W2Z9	Q8w2z9 oryza sativ
33	39	32.2	688	16	O25812	O25812 helicobacte
34	39	32.2	688	16	Q9ZK11	Q9zk11 helicobacte
35	39	32.2	1649	16	Q9CFA2	Q9cfa2 lactococcus
36	38.5	31.8	472	16	Q9KZK2	Q9kzk2 streptomyce
37	38.5	31.8	653	10	Q41729	Q41729 zea mays (m
38	38.5	31.8	1702	11	O54875	O54875 rattus norv
39	38	31.4	214	12	Q9PZU6	Q9pzu6 hepatitis d
40	38	31.4	239	10	Q9LTV4	Q9ltv4 arabidopsis
41	38	31.4	241	5	Q04317	Q04317 scaptomyza
42	38	31.4	241	5	Q99183	Q99183 scaptomyza
43	38	31.4	274	16	Q8UDB8	Q8udb8 agrobacteri
44	38	31.4	421	9	Q9XJM0	Q9xjm0 bacteriopha
45	38	31.4	421	9	Q8SC87	Q8sc87 stx2 conver

ALIGNMENTS

RESULT 1
Q9NM02
ID Q9NM02 PRELIMINARY; PRT; 234 AA.
AC Q9NM02;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Possible hypothetical 45.5 kDa protein (Fragment).
GN LM26.290.
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL160493; CAB97908.1; -.
FT NON_TER 234 234
SQ SEQUENCE 234 AA; 24954 MW; 0F013FAB8A1196FA CRC64;

Query Match 36.4%; Score 44; DB 5; Length 234;
Best Local Similarity 44.4%; Pred. No. 4;
Matches 12; Conservative 3; Mismatches 10; Indels 2; Gaps 1;

```
Qy         11 SKQXEEEAV--RLXXXXLKNGGXSSGA 35
              |:|  |:|:   |    | |||  |||
Db        148 SRQVREKALAAMLSEDALVNGGAPSGA 174
```

RESULT 2
P89451
ID P89451 PRELIMINARY; PRT; 785 AA.
AC P89451;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE UL28 protein.
GN UL28.

Search completed: June 24, 2003, 23:05:18
Job time : 50.5 secs

PI Beeley NRA, Prickett KS;
XX
DR WPI; 1999-394773/33.
XX
PT New exendin agonist peptides - can regulate gastric motility and
PT slow gastric emptying, used for treating, e.g. diabetes
XX
PS Claim 18; Fig 4; 108pp; English.
XX
CC AAY24809 to AAY24877 represent exendin agonist peptides which can
CC regulate gastric motility and slow gastric emptying. The peptides can be
CC used for treating e.g. diabetes or hyperglycaemic or hypoglycaemic
CC conditions. The peptides are exendin agonists which have activity as
CC agents to regulate gastric motility and to slow gastric emptying, as
CC evidenced by the ability to reduce post-prandial glucose levels in
CC mammals. They can be used for the treatment of Type I and II diabetes and
CC hyperglycaemic or hypoglycaemic conditions. They can also be used for the
CC treatment of disorders which would be benefited by agents which lower
CC plasma glucose levels and in treatment of disorders which would be
CC benefited with agents useful in delaying and/or slowing gastric
CC emptying.
XX
SQ Sequence 37 AA;

Query Match 76.9%; Score 93; DB 20; Length 37;
Best Local Similarity 65.6%; Pred. No. 6.7e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
|| ||| ||||||| ||||| ||||
Db 4 GTFTSDLSKQMEEEAVRLFIEWLKNGGASSGA 35

RESULT 14
AAY24854
ID AAY24854 standard; peptide; 37 AA.
XX
AC AAY24854;
XX
DT 24-AUG-1999 (first entry)
XX
DE Exendin agonist peptide #46.
XX
KW Exendin; agonist; Heloderma sp.; Gila monster; venom; lizard;
KW diabetes mellitus type I; diabetes mellitus type II; hyperglycaemia;
KW hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.
XX
OS Synthetic.
OS Heloderma sp.
XX
PN WO9925727-A2.
XX
PD 27-MAY-1999.
XX
PF 13-NOV-1998; 98WO-US24210.
XX
PR 14-NOV-1997; 97US-0065442.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Beeley NRA, Prickett KS;
XX
DR WPI; 1999-394773/33.
XX
PT New exendin agonist peptides - can regulate gastric motility and
PT slow gastric emptying, used for treating, e.g. diabetes
XX
PS Claim 18; Fig 4; 108pp; English.
XX
CC AAY24809 to AAY24877 represent exendin agonist peptides which can
CC regulate gastric motility and slow gastric emptying. The peptides can be
CC used for treating e.g. diabetes or hyperglycaemic or hypoglycaemic
CC conditions. The peptides are exendin agonists which have activity as
CC agents to regulate gastric motility and to slow gastric emptying, as
CC evidenced by the ability to reduce post-prandial glucose levels in
CC mammals. They can be used for the treatment of Type I and II diabetes and
CC hyperglycaemic or hypoglycaemic conditions. They can also be used for the
CC treatment of disorders which would be benefited by agents which lower
CC plasma glucose levels and in treatment of disorders which would be
CC benefited with agents useful in delaying and/or slowing gastric
CC emptying.
XX
SQ Sequence 37 AA;

Query Match 76.9%; Score 93; DB 20; Length 37;
Best Local Similarity 65.6%; Pred. No. 6.7e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
|| ||| ||||||| ||||| ||||
Db 4 GTFTSDLSKQMEEEAVRLFIEWLKNGGASSGA 35

RESULT 15
AAB11275
ID AAB11275 standard; Peptide; 37 AA.
XX
AC AAB11275;
XX
DT 20-FEB-2001 (first entry)
XX
DE exendin agonist peptide SEQ ID NO 183.
XX
KW Exendin; agonist; treatment; antidiabetic; insulin sensitivity; diabetes;
KW plasma glucose; gastric emptying; food intake.
XX
OS Synthetic.
XX
PN WO200041546-A2.
XX
PD 20-JUL-2000.
XX
PF 10-JAN-2000; 2000US-0116380.
XX
PR 14-JAN-1999; 99US-0116380.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Young A, L'Italien JJ, Kolterman O;
XX
DR WPI; 2000-514584/46.
XX
PT New formulations comprising an exendin or exendin agonist peptide used
PT for increasing the sensitivity of a subject to insulin to treat
PT diabetes -
XX
PS Example 192; Page 238; 281pp; English.
XX
CC This invention describes a novel formulation (I) comprising an exendin or
CC exendin agonist peptide, a buffer and an iso-osmolality modifier which
CC has a pH of 3-7. The products of the invention have antidiabetic
CC activity. The exendin or exendin agonist is used to increase the
CC sensitivity of a subject to insulin to treat diabetes and disorders which
CC would benefit from agents which lower plasma glucose levels and disorders
CC which would benefit from agents that delay and/or slow gastric emptying
CC or reducing food intake.
XX
SQ Sequence 37 AA;

Query Match 76.9%; Score 93; DB 21; Length 37;
Best Local Similarity 68.8%; Pred. No. 6.7e-10;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
|| ||| ||||||| |||||||||
Db 4 GTFTSALSKQMEEEAVRLFIEWLKNGGXSSGA 35

OS Synthetic.
XX
PN WO200073331-A2.
XX
PD 07-DEC-2000.
XX
PF 23-MAY-2000; 2000WO-US14231.
XX
PR 01-JUN-1999; 99US-0323867.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Hiles R, Prickett KS;
XX
DR WPI; 2001-137634/14.
XX
PT Use of exendins or exendin agonists for lowering or reducing blood
PT glucose levels and treating gestational diabetes mellitus in a subject,
PT especially in a human -
XX
PS Example 166; Page 113; 133pp; English.
XX
CC The invention relates to the use of an exendin (AAB64181-B64182) or
CC an exendin agonist (AAB64185-B64368) for treating gestational diabetes
CC mellitus (GDM) in a patient. GDM arises during pregnancy, and is due
CC to a combination of increased insulin resistance and a diminished
CC ability to increase insulin secretion. In contrast, in a normal
CC pregnancy, both insulin resistance and insulin secretion increase. GDM
CC pregnancies are associated with complications in both the mother and the
CC foetus. Women with GDM have increased rates of Caesarian delivery,
CC hypertensive disorders such as pre-eclampsia, and urinary tract
CC infections. GDM results in an elevated rate of foetal abnormalities such
CC as neural tube defects, and is associated with an increased risk of
CC neonatal morbidites such as hypoglycaemia, hypocalcaemia,
CC hypomagnesaemia, polycythaemia, hyperbilirubinaemia, and subsequent
CC childhood and adolescent obesity. Exendins are peptides from the salivary
CC secretions of the Gila monster (exendin-4) and the Mexican beaded lizard
CC (exendin-3) which exhibit homology with several members of the
CC glucagon-like peptide family, particularly GLP-1, and have similar
CC insulinotropic effects. Unlike the compounds used to treat type 2
CC diabetes, which are contraindicated for GDM, exendins and exendin
CC agonists do not cross the placenta and thus do not cause severe prolonged
CC hypoglycaemia in the newborn. They have a potent and prolonged effect on
CC blood glucose, and, unlike conventional insulin therapy, should not cause
CC weight gain, as they inhibit gastric emptying and reduce appetite. The
CC present sequence represents a exendin agonist of the invention which is
CC based upon the sequence of exendin-4.
XX
SQ Sequence 36 AA;

Query Match 76.9%; Score 93; DB 22; Length 36;
Best Local Similarity 65.6%; Pred. No. 6.5e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
|| ||| ||||||| ||||| ||||
Db 4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35

RESULT 12
AAY24869
ID AAY24869 standard; peptide; 37 AA.
XX
AC AAY24869;
XX
DT 24-AUG-1999 (first entry)
XX
DE Exendin agonist peptide #61.
XX
KW Exendin; agonist; Heloderma sp.; Gila monster; venom; lizard;
KW diabetes mellitus type I; diabetes mellitus type II; hyperglycaemia;
KW hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.
XX

OS Synthetic.
OS Heloderma sp.
XX
PN WO9925727-A2.
XX
PD 27-MAY-1999.
XX
PF 13-NOV-1998; 98WO-US24210.
XX
PR 14-NOV-1997; 97US-0065442.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Beeley NRA, Prickett KS;
XX
DR WPI; 1999-394773/33.
XX
PT New exendin agonist peptides - can regulate gastric motility and
PT slow gastric emptying, used for treating, e.g. diabetes
XX
PS Claim 18; Fig 4; 108pp; English.
XX
CC AAY24809 to AAY24877 represent exendin agonist peptides which can
CC regulate gastric motility and slow gastric emptying. The peptides can be
CC used for treating e.g. diabetes or hyperglycaemic or hypoglycaemic
CC conditions. The peptides are exendin agonists which have activity as
CC agents to regulate gastric motility and to slow gastric emptying, as
CC evidenced by the ability to reduce post-prandial glucose levels in
CC mammals. They can be used for the treatment of Type I and II diabetes and
CC hyperglycaemic or hypoglycaemic conditions. They can also be used for the
CC treatment of disorders which would be benefited by agents which lower
CC plasma glucose levels and in treatment of disorders which would be
CC benefited with agents useful in delaying and/or slowing gastric
CC emptying.
XX
SQ Sequence 37 AA;

Query Match 76.9%; Score 93; DB 20; Length 37;
Best Local Similarity 68.8%; Pred. No. 6.7e-10;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
|| ||| ||||||| ||||||||||
Db 4 GTFTSDASKQMEEEAVRLFIEWLKNGGXSSGA 35

RESULT 13
AAY24853
ID AAY24853 standard; peptide; 37 AA.
XX
AC AAY24853;
XX
DT 24-AUG-1999 (first entry)
XX
DE Exendin agonist peptide #45.
XX
KW Exendin; agonist; Heloderma sp.; Gila monster; venom; lizard;
KW diabetes mellitus type I; diabetes mellitus type II; hyperglycaemia;
KW hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.
XX
OS Synthetic.
OS Heloderma sp.
XX
PN WO9925727-A2.
XX
PD 27-MAY-1999.
XX
PF 13-NOV-1998; 98WO-US24210.
XX
PR 14-NOV-1997; 97US-0065442.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX

```
Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| ||||||||    ||||| ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35
```

RESULT 9
AAY94184
ID AAY94184 standard; peptide; 36 AA.
XX
AC AAY94184;
XX
DT 20-OCT-2000 (first entry)
XX
DE Amino acid sequence of an extendin agonist.
XX
KW Extendin; Gila monster lizard; Mexican Beaded lizard; agonist;
KW glucagon-like peptide; plasma glucagon; necrolytic erythema;
KW glucagonoma; hyperglucagonemia; diabetes.
XX
OS Synthetic.
OS Heloderma sp.
XX
FH Key Location/Qualifiers
FT Modified-site 36
FT /note= "amidated residue"
XX
PN WO200041548-A2.
XX
PD 20-JUL-2000.
XX
PF 14-JAN-2000; 2000WO-US00942.
XX
PR 14-JAN-1999; 99US-0116380.
PR 30-APR-1999; 99US-0132017.
PR 10-JAN-2000; 2000US-0175365.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Young A, Gedulin B;
XX
DR WPI; 2000-490999/43.
XX
PT Lowering plasma glucagon using exendin, an exendin agonist, a modified
PT exendin or a modified exendin agonist, useful for treating
PT hyperglucagonemia and diabetes -
XX
PS Disclosure; Fig 4G; 96pp; English.
XX
CC The present sequence represents a modified extendin or extendin agonist.
CC Extendins are found in the salivary glands of the Gila monster and
CC Mexican Beaded lizard, and have sequence similarity to glucagon-like
CC peptides. They are used in the method of the invention. The specification
CC describes a method for lowering plasma glucagon, comprising administering
CC an exendin, an exendin agonist, a modified exendin or a modified exendin
CC agonist. These compounds lower plasma glucagon level. The method is
CC useful for lowering plasma glucagon in subjects, preferably humans,
CC suffering from necrolytic erythema or glucagonoma. The method is also
CC useful for treating hyperglucagonemia and other conditions that would
CC benefit from reduced glucagon levels and/or suppression of glucagon,
CC e.g. type 1 and type 2 diabetes.
XX
SQ Sequence 36 AA;

Query Match 76.9%; Score 93; DB 21; Length 36;
Best Local Similarity 65.6%; Pred. No. 6.5e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

```
Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| ||||||||    ||||| ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35
```

RESULT 10
AAE08515
ID AAE08515 standard; peptide; 36 AA.
XX
AC AAE08515;
XX
DT 01-NOV-2001 (first entry)
XX
DE Exendin agonist peptide #160.
XX
KW Exendin agonist; antilipemic; cardiant; triglyceride; inotropic;
KW diuretic; coronary heart disease; dyslipidaemia.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 36
FT /note= "C-terminal amide"
XX
PN WO200151078-A1.
XX
PD 19-JUL-2001.
XX
PF 09-JAN-2001; 2001WO-US00719.
XX
PR 10-JAN-2000; 2000US-0175365.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Kolterman OG, Young AA;
XX
DR WPI; 2001-514422/56.
XX
PT Use of exendin and exendin agonist compounds for modulating
PT triglyceride levels, and treating heart disease and dyslipidemia -
XX
PS Example 166; Page 136; 161pp; English.
XX
CC The patent discloses a method for modulating plasma or postprandial
CC triglyceride and other lipid levels by administering exendin or an
CC exendin agonist. Exendins have inotropic and diuretic effects. They
CC suppress the secretion of glucagon. Exendin and its agonists have
CC a significant effect on the reduction of blood serum triglyceride
CC concentrations. They are used to treat coronary heart disease and
CC dyslipidaemia, and for modifying postprandial triglyceride levels.
CC The present peptide sequence is an agonist of exendin.
XX
SQ Sequence 36 AA;

Query Match 76.9%; Score 93; DB 22; Length 36;
Best Local Similarity 65.6%; Pred. No. 6.5e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

```
Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| ||||||||    ||||| ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35
```

RESULT 11
AAB64351
ID AAB64351 standard; peptide; 36 AA.
XX
AC AAB64351;
XX
DT 27-MAR-2001 (first entry)
XX
DE Exendin agonist, SEQ ID NO:171.
XX
KW Exendin agonist; gestational diabetes mellitus; GDM; insulin resistance;
KW pregnancy complication; neonatal abnormality; blood glucose modulator;
KW insulinotropic; anorectic; exendin-4.
XX
OS Heloderma suspectum.

KW diabetes mellitus type I; diabetes mellitus type II; hyperglycaemia;
KW hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.
XX
OS Synthetic.
OS Heloderma sp.
XX
PN WO9925728-A1.
XX
PD 27-MAY-1999.
XX
PF 13-NOV-1998; 98WO-US24273.
XX
PR 14-NOV-1997; 97US-0066029.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Beeley NRA, Prickett KS;
XX
DR WPI; 1999-347456/29.
XX
PT Peptide agonists of exendin - delay stomach emptying, for treating
PT diabetes and hypo- or hyper-glycaemia
XX
PS Claim 28; Fig 4; 144pp; English.
XX
CC AAY17535 to AAY17624 represent exendin peptide agonists. Exendins are
CC peptides that are found in the venom of the Gila-monster, a lizard
CC endogenous to Arizona and Northern Mexico. The peptide agonists are
CC used to treat diabetes mellitus (types I or II), hyperglycaemia or
CC hypoglycaemia. They can also be used for in vitro and in vivo studies
CC on exendins and their agonists. They regulate gastric motility and slow
CC gastric emptying (resulting in lower post-prandial glucose levels).
XX
SQ Sequence 36 AA;

Query Match 76.9%; Score 93; DB 20; Length 36;
Best Local Similarity 65.6%; Pred. No. 6.5e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
|| ||| ||||||| ||||| ||||
Db 4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35

RESULT 7
AAB11263
ID AAB11263 standard; Peptide; 36 AA.
XX
AC AAB11263;
XX
DT 20-FEB-2001 (first entry)
XX
DE exendin agonist peptide SEQ ID NO 171.
XX
KW Exendin; agonist; treatment; antidiabetic; insulin sensitivity; diabetes;
KW plasma glucose; gastric emptying; food intake.
XX
OS Synthetic.
XX
PN WO200041546-A2.
XX
PD 20-JUL-2000.
XX
PF 10-JAN-2000; 2000US-0116380.
XX
PR 14-JAN-1999; 99US-0116380.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Young A, L'Italien JJ, Kolterman O;
XX
DR WPI; 2000-514584/46.
XX
PT New formulations comprising an exendin or exendin agonist peptide used
PT for increasing the sensitivity of a subject to insulin to treat
PT diabetes -
XX
PS Example 180; Page 229; 281pp; English.
XX
CC This invention describes a novel formulation (I) comprising an exendin or
CC exendin agonist peptide, a buffer and an iso-osmolality modifier which
CC has a pH of 3-7. The products of the invention have antidiabetic
CC activity. The exendin or exendin agonist is used to increase the
CC sensitivity of a subject to insulin to treat diabetes and disorders which
CC would benefit from agents which lower plasma glucose levels and disorders
CC which would benefit from agents that delay and/or slow gastric emptying
CC or reducing food intake.
XX
SQ Sequence 36 AA;

Query Match 76.9%; Score 93; DB 21; Length 36;
Best Local Similarity 65.6%; Pred. No. 6.5e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
|| ||| ||||||| ||||| ||||
Db 4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35

RESULT 8
AAB53029
ID AAB53029 standard; Peptide; 36 AA.
XX
AC AAB53029;
XX
DT 28-FEB-2001 (first entry)
XX
DE Extendin agonist compound #157.
XX
KW Extendin; agonist; diabetes; obesity; eating disorder;
KW dyslipidaemia; insulin-resistance syndrome; food intake.
XX
OS Heloderma sp.
XX
PN WO200066629-A1.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US11814.
XX
PR 30-APR-1999; 99US-0132018.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Young A, Prickett K;
XX
DR WPI; 2000-672834/65.
XX
PT Modified exendin or an exendin agonist linked to one or more
PT polyethylene glycol (PEG) polymers, modulate plasma glucose levels,
PT useful for treating disorders such as diabetes and obesity -
XX
PS Disclosure; Fig 4; 119pp; English.
XX
CC The present invention relates to extendins and their agonists which have
CC been modified with molecular weight increasing agents such as
CC polyethylene glycol (PEG). These can be used in the treatment of
CC diabetes, obesity, impaired glucose tolerance, postprandial dumping
CC syndrome, postprandial hyperglycaemia, eating disorders, insulin
CC resistance syndrome, dyslipidaemia and to suppress glucagon secretion.
XX
SQ Sequence 36 AA;

Query Match 76.9%; Score 93; DB 21; Length 36;
Best Local Similarity 65.6%; Pred. No. 6.5e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

```
XX
SQ   Sequence   37 AA;

  Query Match            77.7%;  Score 94;  DB 22;  Length 37;
  Best Local Similarity   65.6%;  Pred. No. 4.4e-10;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| ||||||| |||||  ||||
Db          4 GTFTSALSKQMEEEAVRLFIEWLKNGGASSGA 35


RESULT 4
AAB11313
ID   AAB11313 standard; Peptide; 39 AA.
XX
AC   AAB11313;
XX
DT   20-FEB-2001  (first entry)
XX
DE   exendin agonist peptide SEQ ID NO 39.
XX
KW   Exendin; agonist; treatment; antidiabetic; insulin sensitivity; diabetes;
KW   plasma glucose; gastric emptying; food intake.
XX
OS   Synthetic.
XX
PN   WO200041546-A2.
XX
PD   20-JUL-2000.
XX
PF   10-JAN-2000; 2000US-0116380.
XX
PR   14-JAN-1999;   99US-0116380.
XX
PA   (AMYL-) AMYLIN PHARM INC.
XX
PI   Young A,  L'Italien JJ,  Kolterman O;
XX
DR   WPI; 2000-514584/46.
XX
PT   New formulations comprising an exendin or exendin agonist peptide used
PT   for increasing the sensitivity of a subject to insulin to treat
PT   diabetes -
XX
PS   Example 44; Figure 15; 281pp; English.
XX
CC   This invention describes a novel formulation (I) comprising an exendin or
CC   exendin agonist peptide, a buffer and an iso-osmolality modifier which
CC   has a pH of 3-7. The products of the invention have antidiabetic
CC   activity. The exendin or exendin agonist is used to increase the
CC   sensitivity of a subject to insulin to treat diabetes and disorders which
CC   would benefit from agents which lower plasma glucose levels and disorders
CC   which would benefit from agents that delay and/or slow gastric emptying
CC   or reducing food intake.
XX
SQ   Sequence   39 AA;

  Query Match            77.7%;  Score 94;  DB 21;  Length 39;
  Best Local Similarity   65.6%;  Pred. No. 4.7e-10;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| ||||||| |||||  ||||
Db          4 GTFTSDLSKQLEEEAVRLFIEFLKNGGASSGA 35


RESULT 5
AAE08383
ID   AAE08383 standard; peptide; 39 AA.
XX
AC   AAE08383;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Exendin agonist peptide #30.
XX
KW   Exendin agonist; antilipemic; cardiant; triglyceride; inotropic;
KW   diuretic; coronary heart disease; dyslipidaemia.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   31
FT                   /note= "N-Methyl-alanine"
FT   Modified-site   36
FT                   /note= "N-Methyl-alanine"
FT   Modified-site   37
FT                   /note= "N-Methyl-alanine"
FT   Modified-site   38
FT                   /note= "N-Methyl-alanine"
FT   Modified-site   39
FT                   /note= "C-terminal amide"
XX
PN   WO200151078-A1.
XX
PD   19-JUL-2001.
XX
PF   09-JAN-2001; 2001WO-US00719.
XX
PR   10-JAN-2000; 2000US-0175365.
XX
PA   (AMYL-) AMYLIN PHARM INC.
XX
PI   Kolterman OG,  Young AA;
XX
DR   WPI; 2001-514422/56.
XX
PT   Use of exendin and exendin agonist compounds for modulating
PT   triglyceride levels, and treating heart disease and dyslipidemia -
XX
PS   Example 30; Page -; 161pp; English.
XX
CC   The patent discloses a method for modulating plasma or postprandial
CC   triglyceride and other lipid levels by administering exendin or an
CC   exendin agonist. Exendins have inotropic and diuretic effects. They
CC   suppress the secretion of glucagon. Exendin and its agonists have
CC   a significant effect on the reduction of blood serum triglyceride
CC   concentrations. They are used to treat coronary heart disease and
CC   dyslipidaemia, and for modifying postprandial triglyceride levels.
CC   The present peptide sequence is an agonist of exendin.
CC   Note: The present sequence is not shown in the specification but is
CC   derived from SEQ ID NO:3 shown in page 17 of the specification.
XX
SQ   Sequence   39 AA;

  Query Match            77.7%;  Score 94;  DB 22;  Length 39;
  Best Local Similarity   65.6%;  Pred. No. 4.7e-10;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| ||||||| |||||  ||||
Db          4 GTFTSDLSKQLEEEAVRLFIEFLKNGGASSGA 35


RESULT 6
AAY17606
ID   AAY17606 standard; peptide; 36 AA.
XX
AC   AAY17606;
XX
DT   09-AUG-1999  (first entry)
XX
DE   Exendin agonist peptide #72.
XX
KW   Exendin; agonist; Heloderma sp.; Gila monster; venom; lizard;
```

XX
PS Claim 28; Fig 4; 144pp; English.
XX
CC AAY17535 to AAY17624 represent exendin peptide agonists. Exendins are
CC peptides that are found in the venom of the Gila-monster, a lizard
CC endogenous to Arizona and Northern Mexico. The peptide agonists are
CC used to treat diabetes mellitus (types I or II), hyperglycaemia or
CC hypoglycaemia. They can also be used for in vitro and in vivo studies
CC on exendins and their agonists. They regulate gastric motility and slow
CC gastric emptying (resulting in lower post-prandial glucose levels).
XX
SQ Sequence 37 AA;

Query Match 77.7%; Score 94; DB 20; Length 37;
Best Local Similarity 65.6%; Pred. No. 4.4e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
|| ||| ||||||| ||||| ||||
Db 4 GTFTSALSKQMEEEAVRLFIEWLKNGGASSGA 35

RESULT 2
AAE08527
ID AAE08527 standard; peptide; 37 AA.
XX
AC AAE08527;
XX
DT 01-NOV-2001 (first entry)
XX
DE Exendin agonist peptide #172.
XX
KW Exendin agonist; antilipemic; cardiant; triglyceride; inotropic;
KW diuretic; coronary heart disease; dyslipidaemia.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 31
FT /note= "N-methyl alanine"
FT Modified-site 36
FT /note= "N-methyl alanine"
FT Modified-site 37
FT /note= "N-methyl alanine; C-terminal amide"
XX
PN WO200151078-A1.
XX
PD 19-JUL-2001.
XX
PF 09-JAN-2001; 2001WO-US00719.
XX
PR 10-JAN-2000; 2000US-0175365.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Kolterman OG, Young AA;
XX
DR WPI; 2001-514422/56.
XX
PT Use of exendin and exendin agonist compounds for modulating
PT triglyceride levels, and treating heart disease and dyslipidemia
XX
PS Example 178; Page 143; 161pp; English.
XX
CC The patent discloses a method for modulating plasma or postprandial
CC triglyceride and other lipid levels by administering exendin or an
CC exendin agonist. Exendins have inotropic and diuretic effects. They
CC suppress the secretion of glucagon. Exendin and its agonists have
CC a significant effect on the reduction of blood serum triglyceride
CC concentrations. They are used to treat coronary heart disease and
CC dyslipidaemia, and for modifying postprandial triglyceride levels.
CC The present peptide sequence is an agonist of exendin.
XX

SQ Sequence 37 AA;

Query Match 77.7%; Score 94; DB 22; Length 37;
Best Local Similarity 65.6%; Pred. No. 4.4e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
|| ||| ||||||| ||||| ||||
Db 4 GTFTSALSKQMEEEAVRLFIEWLKNGGASSGA 35

RESULT 3
AAB64363
ID AAB64363 standard; peptide; 37 AA.
XX
AC AAB64363;
XX
DT 27-MAR-2001 (first entry)
XX
DE Exendin agonist, SEQ ID NO:183.
XX
KW Exendin agonist; gestational diabetes mellitus; GDM; insulin resistance;
KW pregnancy complication; neonatal abnormality; blood glucose modulator;
KW insulinotropic; anorectic; exendin-4.
XX
OS Heloderma suspectum.
OS Synthetic.
XX
PN WO200073331-A2.
XX
PD 07-DEC-2000.
XX
PF 23-MAY-2000; 2000WO-US14231.
XX
PR 01-JUN-1999; 99US-0323867.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Hiles R, Prickett KS;
XX
DR WPI; 2001-137634/14.
XX
PT Use of exendins or exendin agonists for lowering or reducing blood
PT glucose levels and treating gestational diabetes mellitus in a subject,
PT especially in a human -
XX
PS Example 178; Page 119; 133pp; English.
XX
CC The invention relates to the use of an exendin (AAB64181-B64182) or
CC an exendin agonist (AAB64185-B64368) for treating gestational diabetes
CC mellitus (GDM) in a patient. GDM arises during pregnancy, and is due
CC to a combination of increased insulin resistance and a diminished
CC ability to increase insulin secretion. In contrast, in a normal
CC pregnancy, both insulin resistance and insulin secretion increase. GDM
CC pregnancies are associated with complications in both the mother and the
CC foetus. Women with GDM have increased rates of Caesarian delivery,
CC hypertensive disorders such as pre-eclampsia, and urinary tract
CC infections. GDM results in an elevated rate of foetal abnormalities such
CC as neural tube defects, and is associated with an increased risk of
CC neonatal morbidites such as hypoglycaemia, hypocalcaemia,
CC hypomagnesaemia, polycythaemia, hyperbilirubinaemia, and subsequent
CC childhood and adolescent obesity. Exendins are peptides from the salivary
CC secretions of the Gila monster (exendin-4) and the Mexican beaded lizard
CC (exendin-3) which exhibit homology with several members of the
CC glucagon-like peptide family, particularly GLP-1, and have similar
CC insulinotropic effects. Unlike the compounds used to treat type 2
CC diabetes, which are contraindicated for GDM, exendins and exendin
CC agonists do not cross the placenta and thus do not cause severe prolonged
CC hypoglycaemia in the newborn. They have a potent and prolonged effect on
CC blood glucose, and, unlike conventional insulin therapy, should not cause
CC weight gain, as they inhibit gastric emptying and reduce appetite. The
CC present sequence represents a exendin agonist of the invention which is
CC based upon the sequence of exendin-4.

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OM protein - protein search, using sw model

Run on: June 24, 2003, 22:59:19 ; Search time 49.5 Seconds
(without alignments)
107.677 Million cell updates/sec

Title: US-09-889-331A-47
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Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	94	77.7	37	20	AAY17618	Exendin agonist pe
2	94	77.7	37	22	AAE08527	Exendin agonist pe
3	94	77.7	37	22	AAB64363	Exendin agonist, S
4	94	77.7	39	21	AAB11313	exendin agonist pe
5	94	77.7	39	22	AAE08383	Exendin agonist pe
6	93	76.9	36	20	AAY17606	Exendin agonist pe
7	93	76.9	36	21	AAB11263	exendin agonist pe
8	93	76.9	36	21	AAB53029	Extendin agonist c
9	93	76.9	36	21	AAY94184	Amino acid sequenc
10	93	76.9	36	22	AAE08515	Exendin agonist pe
11	93	76.9	36	22	AAB64351	Exendin agonist, S
12	93	76.9	37	20	AAY24869	Exendin agonist pe
13	93	76.9	37	20	AAY24853	Exendin agonist pe
14	93	76.9	37	20	AAY24854	Exendin agonist pe
15	93	76.9	37	21	AAB11275	exendin agonist pe
16	93	76.9	37	21	AAB53041	Extendin agonist c
17	93	76.9	37	21	AAY94196	Amino acid sequenc
18	93	76.9	37	22	AAE08427	Exendin agonist pe
19	93	76.9	37	22	AAE08428	Exendin agonist pe
20	93	76.9	37	22	AAE08443	Exendin agonist pe
21	93	76.9	37	22	AAB64263	Exendin agonist, S
22	93	76.9	37	22	AAB64264	Exendin agonist, S
23	93	76.9	37	22	AAB64279	Exendin agonist, S
24	93	76.9	39	21	AAB11311	exendin agonist pe
25	93	76.9	39	21	AAY94039	Amino acid sequenc
26	93	76.9	39	21	AAY94040	Amino acid sequenc
27	93	76.9	39	21	AAY94043	Amino acid sequenc
28	93	76.9	39	22	AAE08379	Exendin agonist pe
29	93	76.9	39	22	AAE08380	Exendin agonist pe
30	93	76.9	39	22	AAE08381	Exendin agonist pe
31	93	76.9	39	22	AAB64219	Exendin agonist, S
32	92	76.0	35	20	AAY31535	Exendin agonist pe
33	92	76.0	35	20	AAY24839	Exendin agonist pe
34	92	76.0	35	20	AAY17608	Exendin agonist pe
35	92	76.0	35	21	AAB11161	exendin agonist pe
36	92	76.0	35	21	AAB11265	exendin agonist pe
37	92	76.0	35	21	AAB52920	Extendin agonist c
38	92	76.0	35	21	AAB53031	Extendin agonist c
39	92	76.0	35	21	AAY94074	Amino acid sequenc
40	92	76.0	35	21	AAY94186	Amino acid sequenc
41	92	76.0	35	22	AAE08413	Exendin agonist pe
42	92	76.0	35	22	AAE08517	Exendin agonist pe
43	92	76.0	35	22	AAB64249	Exendin agonist, S
44	92	76.0	35	22	AAB64353	Exendin agonist, S
45	92	76.0	36	20	AAY31533	Exendin agonist pe

ALIGNMENTS

RESULT 1
AAY17618
ID AAY17618 standard; peptide; 37 AA.
XX
AC AAY17618;
XX
DT 09-AUG-1999 (first entry)
XX
DE Exendin agonist peptide #84.
XX
KW Exendin; agonist; Heloderma sp.; Gila monster; venom; lizard;
KW diabetes mellitus type I; diabetes mellitus type II; hyperglycaemia;
KW hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.
XX
OS Synthetic.
OS Heloderma sp.
XX
PN WO9925728-A1.
XX
PD 27-MAY-1999.
XX
PF 13-NOV-1998; 98WO-US24273.
XX
PR 14-NOV-1997; 97US-0066029.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Beeley NRA, Prickett KS;
XX
DR WPI; 1999-347456/29.
XX
PT Peptide agonists of exendin - delay stomach emptying, for treating
PT diabetes and hypo- or hyper-glycaemia

```
;   NAME/KEY: MOD_RES
;   LOCATION: 40
;   OTHER INFORMATION: Xaa represents Lys(E-MPA)-NH2-5TFA and where "E" represents Epsil
US-09-623-618B-31

  Query Match             61.2%;  Score 68.5;  DB 4;  Length 40;
  Best Local Similarity   59.4%;  Pred. No. 2.5e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 14
US-09-623-618B-32
; Sequence 32, Application US/09623618B
; Patent No. 6329336
; GENERAL INFORMATION:
;  APPLICANT: Bridon, Dominique P.
;  APPLICANT:  L'Archeveque, Benoit
;  APPLICANT:  Ezrin, Alan M.
;  APPLICANT:  Holmes, Darren L.
;  APPLICANT:  Leblanc, Anouk
;  APPLICANT:  St. Pierre, Serge
;  TITLE OF INVENTION: LONG LASTING INSULINOTROPIC PEPTIDES
;  FILE REFERENCE: 500862001620
;  CURRENT APPLICATION NUMBER: US/09/623,618B
;  CURRENT FILING DATE:  2000-09-05
;  PRIOR APPLICATION NUMBER: PCT/US00/13563
;  PRIOR FILING DATE: 2000-05-17
;  PRIOR APPLICATION NUMBER: 60/159,783
;  PRIOR FILING DATE: 1999-10-15
;  PRIOR APPLICATION NUMBER: 60/134,406
;  PRIOR FILING DATE: 1999-05-17
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
;   NAME/KEY: MOD_RES
;   LOCATION: 40
;   OTHER INFORMATION: Xaa represents Lys(E-AEEA-AEEA-MPA)-NH2-5TFA and where "E" repres
US-09-623-618B-32

  Query Match             61.2%;  Score 68.5;  DB 4;  Length 40;
  Best Local Similarity   59.4%;  Pred. No. 2.5e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 15
US-09-623-618B-33
; Sequence 33, Application US/09623618B
; Patent No. 6329336
; GENERAL INFORMATION:
;  APPLICANT: Bridon, Dominique P.
;  APPLICANT:  L'Archeveque, Benoit
;  APPLICANT:  Ezrin, Alan M.
;  APPLICANT:  Holmes, Darren L.
;  APPLICANT:  Leblanc, Anouk
;  APPLICANT:  St. Pierre, Serge
;  TITLE OF INVENTION: LONG LASTING INSULINOTROPIC PEPTIDES
;  FILE REFERENCE: 500862001620
;  CURRENT APPLICATION NUMBER: US/09/623,618B
;  CURRENT FILING DATE:  2000-09-05
;  PRIOR APPLICATION NUMBER: PCT/US00/13563
;  PRIOR FILING DATE: 2000-05-17
;  PRIOR APPLICATION NUMBER: 60/159,783
;  PRIOR FILING DATE: 1999-10-15
;  PRIOR APPLICATION NUMBER: 60/134,406
;  PRIOR FILING DATE: 1999-05-17
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
;   NAME/KEY: MOD_RES
;   LOCATION: 40
;   OTHER INFORMATION: Xaa represents Lys(E-MPA)-NH2-5TFA and where "E" represents Ep
US-09-623-618B-33

  Query Match             61.2%;  Score 68.5;  DB 4;  Length 40;
  Best Local Similarity   59.4%;  Pred. No. 2.5e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


Search completed: June 24, 2003, 23:09:16
Job time : 17.5 secs
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RESULT 10
US-09-303-016-9
; Sequence 9, Application US/09303016
; Patent No. 6429197
; GENERAL INFORMATION:
;  APPLICANT:  Coolidge, Thomas R.
;  APPLICANT:  Ehlers, Mario R.W.
;  TITLE OF INVENTION:  Metabolic Intervention with GLP-1 or its Biologically
;  TITLE OF INVENTION:  Active Analogues to Improve the Function of the
;  TITLE OF INVENTION:  Ischemic and Reperfused Brain
;  FILE REFERENCE:  P03660US2
;  CURRENT APPLICATION NUMBER: US/09/303,016
;  CURRENT FILING DATE:  1999-04-30
;  PRIOR APPLICATION NUMBER:  60/103,498
;  PRIOR FILING DATE:  1998-10-08
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 39
;   TYPE: PRT
;   ORGANISM: Heloderma suspectum
US-09-303-016-9

  Query Match             61.2%;  Score 68.5;  DB 4;  Length 39;
  Best Local Similarity   59.4%;  Pred. No. 2.4e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 11
US-09-623-618B-18
; Sequence 18, Application US/09623618B
; Patent No. 6329336
; GENERAL INFORMATION:
;  APPLICANT: Bridon, Dominique P.
;  APPLICANT:  L'Archeveque, Benoit
;  APPLICANT:  Ezrin, Alan M.
;  APPLICANT:  Holmes, Darren L.
;  APPLICANT:  Leblanc, Anouk
;  APPLICANT:  St. Pierre, Serge
;  TITLE OF INVENTION: LONG LASTING INSULINOTROPIC PEPTIDES
;  FILE REFERENCE: 500862001620
;  CURRENT APPLICATION NUMBER: US/09/623,618B
;  CURRENT FILING DATE:  2000-09-05
;  PRIOR APPLICATION NUMBER: PCT/US00/13563
;  PRIOR FILING DATE: 2000-05-17
;  PRIOR APPLICATION NUMBER: 60/159,783
;  PRIOR FILING DATE: 1999-10-15
;  PRIOR APPLICATION NUMBER: 60/134,406
;  PRIOR FILING DATE: 1999-05-17
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-09-623-618B-18

  Query Match             61.2%;  Score 68.5;  DB 4;  Length 40;
  Best Local Similarity   59.4%;  Pred. No. 2.5e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 12
US-09-623-618B-19
; Sequence 19, Application US/09623618B
; Patent No. 6329336
; GENERAL INFORMATION:
;  APPLICANT: Bridon, Dominique P.
;  APPLICANT:  L'Archeveque, Benoit
;  APPLICANT:  Ezrin, Alan M.
;  APPLICANT:  Holmes, Darren L.
;  APPLICANT:  Leblanc, Anouk
;  APPLICANT:  St. Pierre, Serge
;  TITLE OF INVENTION: LONG LASTING INSULINOTROPIC PEPTIDES
;  FILE REFERENCE: 500862001620
;  CURRENT APPLICATION NUMBER: US/09/623,618B
;  CURRENT FILING DATE:  2000-09-05
;  PRIOR APPLICATION NUMBER: PCT/US00/13563
;  PRIOR FILING DATE: 2000-05-17
;  PRIOR APPLICATION NUMBER: 60/159,783
;  PRIOR FILING DATE: 1999-10-15
;  PRIOR APPLICATION NUMBER: 60/134,406
;  PRIOR FILING DATE: 1999-05-17
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-09-623-618B-19

  Query Match             61.2%;  Score 68.5;  DB 4;  Length 40;
  Best Local Similarity   59.4%;  Pred. No. 2.5e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 13
US-09-623-618B-31
; Sequence 31, Application US/09623618B
; Patent No. 6329336
; GENERAL INFORMATION:
;  APPLICANT: Bridon, Dominique P.
;  APPLICANT:  L'Archeveque, Benoit
;  APPLICANT:  Ezrin, Alan M.
;  APPLICANT:  Holmes, Darren L.
;  APPLICANT:  Leblanc, Anouk
;  APPLICANT:  St. Pierre, Serge
;  TITLE OF INVENTION: LONG LASTING INSULINOTROPIC PEPTIDES
;  FILE REFERENCE: 500862001620
;  CURRENT APPLICATION NUMBER: US/09/623,618B
;  CURRENT FILING DATE:  2000-09-05
;  PRIOR APPLICATION NUMBER: PCT/US00/13563
;  PRIOR FILING DATE: 2000-05-17
;  PRIOR APPLICATION NUMBER: 60/159,783
;  PRIOR FILING DATE: 1999-10-15
;  PRIOR APPLICATION NUMBER: 60/134,406
;  PRIOR FILING DATE: 1999-05-17
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-09-623-618B-11

  Query Match           61.2%;  Score 68.5;  DB 4;  Length 39;
  Best Local Similarity  59.4%;  Pred. No. 2.4e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 6
US-09-623-618B-12
; Sequence 12, Application US/09623618B
; Patent No. 6329336
; GENERAL INFORMATION:
;  APPLICANT: Bridon, Dominique P.
;  APPLICANT:  L'Archeveque, Benoit
;  APPLICANT:  Ezrin, Alan M.
;  APPLICANT:  Holmes, Darren L.
;  APPLICANT:  Leblanc, Anouk
;  APPLICANT:  St. Pierre, Serge
;  TITLE OF INVENTION: LONG LASTING INSULINOTROPIC PEPTIDES
;  FILE REFERENCE: 500862001620
;  CURRENT APPLICATION NUMBER: US/09/623,618B
;  CURRENT FILING DATE:  2000-09-05
;  PRIOR APPLICATION NUMBER: PCT/US00/13563
;  PRIOR FILING DATE: 2000-05-17
;  PRIOR APPLICATION NUMBER: 60/159,783
;  PRIOR FILING DATE: 1999-10-15
;  PRIOR APPLICATION NUMBER: 60/134,406
;  PRIOR FILING DATE: 1999-05-17
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 39
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-09-623-618B-12

  Query Match           61.2%;  Score 68.5;  DB 4;  Length 39;
  Best Local Similarity  59.4%;  Pred. No. 2.4e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 7
US-09-333-415-7
; Sequence 7, Application US/09333415
; Patent No. 6344180
; GENERAL INFORMATION:
;  APPLICANT:  Holst, Jens J.
;  APPLICANT:  Vilsboll, Tina
;  TITLE OF INVENTION:  GLP-1 as a Diagnostic Test to Determine Beta-Cell
;  TITLE OF INVENTION:  Function and the Presence of the Condition of IGT and
;  TITLE OF INVENTION:  Type-II Diabetes
;  FILE REFERENCE:  P03987US0
;  CURRENT APPLICATION NUMBER: US/09/333,415
;  CURRENT FILING DATE:  1999-06-15
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 39
;   TYPE: PRT
;   ORGANISM: Heloderma suspectum
US-09-333-415-7

  Query Match           61.2%;  Score 68.5;  DB 4;  Length 39;
  Best Local Similarity  59.4%;  Pred. No. 2.4e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 8
US-09-333-415-9
; Sequence 9, Application US/09333415
; Patent No. 6344180
; GENERAL INFORMATION:
;  APPLICANT:  Holst, Jens J.
;  APPLICANT:  Vilsboll, Tina
;  TITLE OF INVENTION:  GLP-1 as a Diagnostic Test to Determine Beta-Cell
;  TITLE OF INVENTION:  Function and the Presence of the Condition of IGT and
;  TITLE OF INVENTION:  Type-II Diabetes
;  FILE REFERENCE:  P03987US0
;  CURRENT APPLICATION NUMBER: US/09/333,415
;  CURRENT FILING DATE:  1999-06-15
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 39
;   TYPE: PRT
;   ORGANISM: Heloderma suspectum
US-09-333-415-9

  Query Match           61.2%;  Score 68.5;  DB 4;  Length 39;
  Best Local Similarity  59.4%;  Pred. No. 2.4e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 9
US-09-303-016-7
; Sequence 7, Application US/09303016
; Patent No. 6429197
; GENERAL INFORMATION:
;  APPLICANT:  Coolidge, Thomas R.
;  APPLICANT:  Ehlers, Mario R.W.
;  TITLE OF INVENTION:  Metabolic Intervention with GLP-1 or its Biologically
;  TITLE OF INVENTION:  Active Analogues to Improve the Function of the
;  TITLE OF INVENTION:  Ischemic and Reperfused Brain
;  FILE REFERENCE:  P03660US2
;  CURRENT APPLICATION NUMBER: US/09/303,016
;  CURRENT FILING DATE:  1999-04-30
;  PRIOR APPLICATION NUMBER:  60/103,498
;  PRIOR FILING DATE:  1998-10-08
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 39
;   TYPE: PRT
;   ORGANISM: Heloderma suspectum
US-09-303-016-7

  Query Match           61.2%;  Score 68.5;  DB 4;  Length 39;
  Best Local Similarity  59.4%;  Pred. No. 2.4e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35
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              ||     ||| |||||||     |  || ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 2
US-08-066-480-2
; Sequence 2, Application US/08066480
; Patent No. 5424286
;  GENERAL INFORMATION:
;    APPLICANT:  Eng, John
;    TITLE OF INVENTION:  Pharmaceutical Compositions And Use of
;    TITLE OF INVENTION:  Exendin-3 and Exendin-4 for Treatment of Diabetes Mellitus
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Allegretti & Witcoff, Ltd.
;      STREET:  10 S. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/066,480
;      FILING DATE:  24-MAR-1993
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McDonnell, John J
;      REGISTRATION NUMBER:  26,949
;      REFERENCE/DOCKET NUMBER:  93,084
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-715-1000
;      TELEFAX:  312-715-1234
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..39
;      OTHER INFORMATION:  /label= Exendin-4
US-08-066-480-2

  Query Match             61.2%;  Score 68.5;  DB 1;  Length 39;
  Best Local Similarity   59.4%;  Pred. No. 2.4e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||     |  || ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 3
US-09-302-596-7
; Sequence 7, Application US/09302596
; Patent No. 6284725
; GENERAL INFORMATION:
;  APPLICANT: Coolidge, Thomas R.
;  APPLICANT:  Ehlers, Mario R.W.
;  TITLE OF INVENTION: Metabolic Intervention with GLP-1 to Improve the Function of
;  TITLE OF INVENTION:  Ischemic and Reperfused Tissue
;  FILE REFERENCE: P03660US1
;  CURRENT APPLICATION NUMBER: US/09/302,596
;  CURRENT FILING DATE:  1999-04-30
;  PRIOR APPLICATION NUMBER: 60/103,498
;  PRIOR FILING DATE: 1998-10-08
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 39
;   TYPE: PRT
;   ORGANISM: Gila Monster venom
US-09-302-596-7

  Query Match             61.2%;  Score 68.5;  DB 4;  Length 39;
  Best Local Similarity   59.4%;  Pred. No. 2.4e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||     |  || ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 4
US-09-302-596-9
; Sequence 9, Application US/09302596
; Patent No. 6284725
; GENERAL INFORMATION:
;  APPLICANT: Coolidge, Thomas R.
;  APPLICANT:  Ehlers, Mario R.W.
;  TITLE OF INVENTION: Metabolic Intervention with GLP-1 to Improve the Function of
;  TITLE OF INVENTION:  Ischemic and Reperfused Tissue
;  FILE REFERENCE: P03660US1
;  CURRENT APPLICATION NUMBER: US/09/302,596
;  CURRENT FILING DATE:  1999-04-30
;  PRIOR APPLICATION NUMBER: 60/103,498
;  PRIOR FILING DATE: 1998-10-08
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 39
;   TYPE: PRT
;   ORGANISM: Gila Monster venom
US-09-302-596-9

  Query Match             61.2%;  Score 68.5;  DB 4;  Length 39;
  Best Local Similarity   59.4%;  Pred. No. 2.4e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||     |  || ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 5
US-09-623-618B-11
; Sequence 11, Application US/09623618B
; Patent No. 6329336
; GENERAL INFORMATION:
;  APPLICANT: Bridon, Dominique P.
;  APPLICANT:  L'Archeveque, Benoit
;  APPLICANT:  Ezrin, Alan M.
;  APPLICANT:  Holmes, Darren L.
;  APPLICANT:  Leblanc, Anouk
;  APPLICANT:  St. Pierre, Serge
;  TITLE OF INVENTION: LONG LASTING INSULINOTROPIC PEPTIDES
;  FILE REFERENCE: 500862001620
;  CURRENT APPLICATION NUMBER: US/09/623,618B
;  CURRENT FILING DATE:  2000-09-05
;  PRIOR APPLICATION NUMBER: PCT/US00/13563
;  PRIOR FILING DATE: 2000-05-17
;  PRIOR APPLICATION NUMBER: 60/159,783
;  PRIOR FILING DATE: 1999-10-15
;  PRIOR APPLICATION NUMBER: 60/134,406
;  PRIOR FILING DATE: 1999-05-17
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 39
;   TYPE: PRT
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OM protein - protein search, using sw model

Run on: June 24, 2003, 23:03:40 ; Search time 17.5 Seconds
(without alignments)
67.252 Million cell updates/sec

Title: US-09-889-331A-48
Perfect score: 112
Sequence: 1 XXXGTXXXXXSKQXEEEAVRLXXXXLXGGXSSGAXXXXXX 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	68.5	61.2	39	1	US-08-066-480-2	Sequence 2, Appli
3	68.5	61.2	39	4	US-09-302-596-7	Sequence 7, Appli
4	68.5	61.2	39	4	US-09-302-596-9	Sequence 9, Appli
5	68.5	61.2	39	4	US-09-623-618B-11	Sequence 11, Appl
6	68.5	61.2	39	4	US-09-623-618B-12	Sequence 12, Appl
7	68.5	61.2	39	4	US-09-333-415-7	Sequence 7, Appli
8	68.5	61.2	39	4	US-09-333-415-9	Sequence 9, Appli
9	68.5	61.2	39	4	US-09-303-016-7	Sequence 7, Appli
10	68.5	61.2	39	4	US-09-303-016-9	Sequence 9, Appli
11	68.5	61.2	40	4	US-09-623-618B-18	Sequence 18, Appl
12	68.5	61.2	40	4	US-09-623-618B-19	Sequence 19, Appl
13	68.5	61.2	40	4	US-09-623-618B-31	Sequence 31, Appl
14	68.5	61.2	40	4	US-09-623-618B-32	Sequence 32, Appl
15	68.5	61.2	40	4	US-09-623-618B-33	Sequence 33, Appl
16	68.5	61.2	40	4	US-09-623-618B-34	Sequence 34, Appl
17	67	59.8	29	4	US-09-623-618B-22	Sequence 22, Appl
18	60.5	54.0	31	1	US-08-066-480-5	Sequence 5, Appli
19	60.5	54.0	31	4	US-09-302-596-8	Sequence 8, Appli
20	60.5	54.0	31	4	US-09-623-618B-15	Sequence 15, Appl
21	60.5	54.0	31	4	US-09-623-618B-24	Sequence 24, Appl
22	60.5	54.0	31	4	US-09-333-415-8	Sequence 8, Appli
23	60.5	54.0	31	4	US-09-303-016-8	Sequence 8, Appli
24	57	50.9	31	1	US-08-066-480-3	Sequence 3, Appli
25	57	50.9	31	1	US-08-066-480-4	Sequence 4, Appli
26	57	50.9	31	4	US-09-623-618B-14	Sequence 14, Appl
27	57	50.9	31	4	US-09-623-618B-23	Sequence 23, Appl
28	57	50.9	32	4	US-09-623-618B-35	Sequence 35, Appl
29	41.5	37.1	31	4	US-09-623-618B-13	Sequence 13, Appl
30	39.5	35.3	30	4	US-09-623-618B-21	Sequence 21, Appl
31	39.5	35.3	31	4	US-09-623-618B-20	Sequence 20, Appl
32	36	32.1	506	4	US-09-134-001C-4383	Sequence 4383, Ap
33	34	30.4	261	1	US-07-971-096-2	Sequence 2, Appli
34	34	30.4	261	1	US-08-175-096-2	Sequence 2, Appli
35	34	30.4	429	1	US-08-339-152A-33	Sequence 33, Appl
36	34	30.4	632	4	US-09-315-127-2	Sequence 2, Appli
37	34	30.4	632	4	US-09-315-127-3	Sequence 3, Appli
38	34	30.4	651	2	US-08-492-027A-1	Sequence 1, Appli
39	34	30.4	655	2	US-08-492-027A-6	Sequence 6, Appli
40	34	30.4	665	4	US-09-309-572-14	Sequence 14, Appl
41	34	30.4	1103	3	US-09-162-373-1	Sequence 1, Appli
42	34	30.4	1103	4	US-09-467-946-1	Sequence 1, Appli
43	33	29.5	220	4	US-09-052-089A-3	Sequence 3, Appli
44	33	29.5	469	2	US-08-968-751-2	Sequence 2, Appli
45	33	29.5	469	4	US-09-052-089A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-066-480-1
; Sequence 1, Application US/08066480
; Patent No. 5424286
; GENERAL INFORMATION:
; APPLICANT: Eng, John
; TITLE OF INVENTION: Pharmaceutical Compositions And Use of
; TITLE OF INVENTION: Exendin-3 and Exendin-4 for Treatment of Diabetes Mellitus
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/066,480
; FILING DATE: 24-MAR-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 93,084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..39
; OTHER INFORMATION: /label= Exendin-3
US-08-066-480-1

Query Match 61.2%; Score 68.5; DB 1; Length 39;
Best Local Similarity 59.4%; Pred. No. 2.4e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34

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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (31)
;   OTHER INFORMATION: tPro
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (36)
;   OTHER INFORMATION: tPro
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (37)
;   OTHER INFORMATION: tPro
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (38)
;   OTHER INFORMATION: tPro
;   FEATURE:
;   OTHER INFORMATION: c-term amidation
US-09-756-690A-36

  Query Match             62.9%;  Score 70.5;  DB 9;  Length 39;
  Best Local Similarity   62.5%;  Pred. No. 3.7e-06;
  Matches   20;  Conservative    0;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  |||||||
Db          4 GTFTSDLSKQLEEEAVRLFIEFLKNGGXSSGA 35


RESULT 15
US-09-756-690A-39
; Sequence 39, Application US/09756690A
; Publication No. US20030036504A1
; GENERAL INFORMATION:
;  APPLICANT: KOLTERMAN, ORVILLE G.
;  APPLICANT:  YOUNG, ANDREW A.
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF
;  TITLE OF INVENTION:  TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
;  FILE REFERENCE: 249/124
;  CURRENT APPLICATION NUMBER: US/09/756,690A
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: PatentIn Ver 2.1
; SEQ ID NO 39
;   LENGTH: 39
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (31)
;   OTHER INFORMATION: MeAla
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (36)
;   OTHER INFORMATION: MeAla
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (37)
;   OTHER INFORMATION: MeAla
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (38)
;   OTHER INFORMATION: MeAla
;   FEATURE:
;   OTHER INFORMATION: c-term amidation
US-09-756-690A-39

  Query Match             62.9%;  Score 70.5;  DB 9;  Length 39;
  Best Local Similarity   62.5%;  Pred. No. 3.7e-06;
  Matches   20;  Conservative    0;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  |||||||
Db          4 GTFTSDLSKQLEEEAVRLFIEFLKNGGXSSGA 35


Search completed: June 24, 2003, 23:20:27
Job time : 31.5 secs
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;  EARLIER FILING DATE: 1997-11-14
;  EARLIER APPLICATION NUMBER: US 60/066,029
;  EARLIER FILING DATE: 1997-11-14
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 99
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificially synthesized sequence of novel exendin agonist
;   OTHER INFORMATION: compound
;   FEATURE:
;   OTHER INFORMATION: Xaa in positions 31, 36 and 37 stands for homoproline.
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (37)...(37)
;   OTHER INFORMATION: amidated hPro (homoprolinamide)
US-09-003-869-99

  Query Match             62.9%;  Score 70.5;  DB 10;  Length 37;
  Best Local Similarity   62.5%;  Pred. No. 3.5e-06;
  Matches   20;  Conservative    0;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  |||||||
Db          4 GTFTSDASKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 12
US-09-003-869-183
; Sequence 183, Application US/09003869A
; Patent No. US20020137666A1
; GENERAL INFORMATION:
;  APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
;  APPLICANT: PRICKETT, KATHRYN S.
;  APPLICANT: BHAVSAR, SUNIL
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
;  TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
;  FILE REFERENCE: 231/181
;  CURRENT APPLICATION NUMBER: US/09/003,869A
;  CURRENT FILING DATE: 1998-01-07
;  EARLIER APPLICATION NUMBER: US 60/034,905
;  EARLIER FILING DATE: 1997-01-07
;  EARLIER APPLICATION NUMBER: US 60/055,404
;  EARLIER FILING DATE: 1997-08-08
;  EARLIER APPLICATION NUMBER: US 60/065,442
;  EARLIER FILING DATE: 1997-11-14
;  EARLIER APPLICATION NUMBER: US 60/066,029
;  EARLIER FILING DATE: 1997-11-14
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 183
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificially synthesized sequence of novel exendin agonist
;   OTHER INFORMATION: compound
;   FEATURE:
;   OTHER INFORMATION: Xaa in positions 31, 36 and 37 stands for n-methylalanine.
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (37)...(37)
;   OTHER INFORMATION: amidated Nmeala (n-methylalaninamide)
US-09-003-869-183

  Query Match             62.9%;  Score 70.5;  DB 10;  Length 37;
  Best Local Similarity   62.5%;  Pred. No. 3.5e-06;
  Matches   20;  Conservative    0;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  |||||||
Db          4 GTFTSALSKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 13
US-09-756-690A-35
; Sequence 35, Application US/09756690A
; Publication No. US20030036504A1
; GENERAL INFORMATION:
;  APPLICANT: KOLTERMAN, ORVILLE G.
;  APPLICANT:  YOUNG, ANDREW A.
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF
;  TITLE OF INVENTION:  TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
;  FILE REFERENCE: 249/124
;  CURRENT APPLICATION NUMBER: US/09/756,690A
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: PatentIn Ver 2.1
; SEQ ID NO 35
;   LENGTH: 39
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (31)
;   OTHER INFORMATION: tPro
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (36)
;   OTHER INFORMATION: tPro
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (37)
;   OTHER INFORMATION: tPro
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (38)
;   OTHER INFORMATION: tPro
;   FEATURE:
;   OTHER INFORMATION: c-term amidation
US-09-756-690A-35

  Query Match             62.9%;  Score 70.5;  DB 9;  Length 39;
  Best Local Similarity   62.5%;  Pred. No. 3.7e-06;
  Matches   20;  Conservative    0;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  |||||||
Db          4 GTFTSDLSKQLEEEAVRLFIEFLKNGGXSSGA 35


RESULT 14
US-09-756-690A-36
; Sequence 36, Application US/09756690A
; Publication No. US20030036504A1
; GENERAL INFORMATION:
;  APPLICANT: KOLTERMAN, ORVILLE G.
;  APPLICANT:  YOUNG, ANDREW A.
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF
;  TITLE OF INVENTION:  TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
;  FILE REFERENCE: 249/124
;  CURRENT APPLICATION NUMBER: US/09/756,690A
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: PatentIn Ver 2.1
; SEQ ID NO 36
;   LENGTH: 39
;   TYPE: PRT
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; SEQ ID NO 183
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
;   FEATURE:
;   OTHER INFORMATION: c-term amidation
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (31)
;   OTHER INFORMATION: N-methylalanine
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (36)..(37)
;   OTHER INFORMATION: N-methylalanine
US-10-157-224A-183

  Query Match             62.9%;  Score 70.5;  DB 9;  Length 37;
  Best Local Similarity   62.5%;  Pred. No. 3.5e-06;
  Matches   20;  Conservative    0;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| ||||||||     |  |||||||
Db          4 GTFTSALSKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 9
US-10-187-051-99
; Sequence 99, Application US/10187051
; Publication No. US20030087821A1
; GENERAL INFORMATION:
;  APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
;  APPLICANT:  PRICKETT, KATHRYN S.
;  APPLICANT:  BHAVSAR, SUNIL
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
;  TITLE OF INVENTION:  THE REDUCTION OF FOOD INTAKE
;  FILE REFERENCE: 231/181
;  CURRENT APPLICATION NUMBER: US/10/187,051
;  CURRENT FILING DATE:  2002-06-28
;  PRIOR APPLICATION NUMBER: US/09/003,869
;  PRIOR FILING DATE: 1998-01-07
;  PRIOR APPLICATION NUMBER: US 60/034,905
;  PRIOR FILING DATE: 1997-01-07
;  PRIOR APPLICATION NUMBER: US 60/055,404
;  PRIOR FILING DATE: 1997-08-08
;  PRIOR APPLICATION NUMBER: US 60/065,442
;  PRIOR FILING DATE: 1997-11-14
;  PRIOR APPLICATION NUMBER: US 60/066,029
;  PRIOR FILING DATE: 1997-11-14
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 99
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificially synthesized sequence of novel exendin
;   OTHER INFORMATION: agonist
;   OTHER INFORMATION: compound
;   FEATURE:
;   OTHER INFORMATION: Xaa in positions 31, 36 and 37 stands for homoproline.
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (37)...(37)
;   OTHER INFORMATION: amidated hPro (homoprolinamide)
US-10-187-051-99

  Query Match             62.9%;  Score 70.5;  DB 9;  Length 37;
  Best Local Similarity   62.5%;  Pred. No. 3.5e-06;
  Matches   20;  Conservative    0;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| ||||||||     |  |||||||
Db          4 GTFTSDASKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 10
US-10-187-051-183
; Sequence 183, Application US/10187051
; Publication No. US20030087821A1
; GENERAL INFORMATION:
;  APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
;  APPLICANT:  PRICKETT, KATHRYN S.
;  APPLICANT:  BHAVSAR, SUNIL
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
;  TITLE OF INVENTION:  THE REDUCTION OF FOOD INTAKE
;  FILE REFERENCE: 231/181
;  CURRENT APPLICATION NUMBER: US/10/187,051
;  CURRENT FILING DATE:  2002-06-28
;  PRIOR APPLICATION NUMBER: US/09/003,869
;  PRIOR FILING DATE: 1998-01-07
;  PRIOR APPLICATION NUMBER: US 60/034,905
;  PRIOR FILING DATE: 1997-01-07
;  PRIOR APPLICATION NUMBER: US 60/055,404
;  PRIOR FILING DATE: 1997-08-08
;  PRIOR APPLICATION NUMBER: US 60/065,442
;  PRIOR FILING DATE: 1997-11-14
;  PRIOR APPLICATION NUMBER: US 60/066,029
;  PRIOR FILING DATE: 1997-11-14
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 183
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificially synthesized sequence of novel exendin
;   OTHER INFORMATION: agonist
;   OTHER INFORMATION: compound
;   FEATURE:
;   OTHER INFORMATION: Xaa in positions 31, 36 and 37 stands for n-
;   OTHER INFORMATION: methylalanine.
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (37)...(37)
;   OTHER INFORMATION: amidated Nmeala (n-methylalaninamide)
US-10-187-051-183

  Query Match             62.9%;  Score 70.5;  DB 9;  Length 37;
  Best Local Similarity   62.5%;  Pred. No. 3.5e-06;
  Matches   20;  Conservative    0;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| ||||||||     |  |||||||
Db          4 GTFTSALSKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 11
US-09-003-869-99
; Sequence 99, Application US/09003869A
; Patent No. US20020137666A1
; GENERAL INFORMATION:
;  APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
;  APPLICANT: PRICKETT, KATHRYN S.
;  APPLICANT: BHAVSAR, SUNIL
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
;  TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
;  FILE REFERENCE: 231/181
;  CURRENT APPLICATION NUMBER: US/09/003,869A
;  CURRENT FILING DATE: 1998-01-07
;  EARLIER APPLICATION NUMBER: US 60/034,905
;  EARLIER FILING DATE: 1997-01-07
;  EARLIER APPLICATION NUMBER: US 60/055,404
;  EARLIER FILING DATE: 1997-08-08
;  EARLIER APPLICATION NUMBER: US 60/065,442
```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (31)
; OTHER INFORMATION: hPro
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (36)
; OTHER INFORMATION: hPro
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (37)
; OTHER INFORMATION: hPro
; FEATURE:
; OTHER INFORMATION: c-term amidation
US-09-756-690A-99

Query Match 62.9%; Score 70.5; DB 9; Length 37;
Best Local Similarity 62.5%; Pred. No. 3.5e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

Qy 4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
|| ||| ||||||| | |||||||
Db 4 GTFTSDASKQMEEEAVRLFIEWLKNGGXSSGA 35

RESULT 6
US-09-756-690A-183
; Sequence 183, Application US/09756690A
; Publication No. US20030036504A1
; GENERAL INFORMATION:
; APPLICANT: KOLTERMAN, ORVILLE G.
; APPLICANT: YOUNG, ANDREW A.
; TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF
; TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
; FILE REFERENCE: 249/124
; CURRENT APPLICATION NUMBER: US/09/756,690A
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/175,365
; PRIOR FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 188
; SOFTWARE: PatentIn Ver 2.1
; SEQ ID NO 183
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (31)
; OTHER INFORMATION: NMeala
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (36)
; OTHER INFORMATION: NMeala
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (37)
; OTHER INFORMATION: NMeala
; FEATURE:
; OTHER INFORMATION: c-term amidation
US-09-756-690A-183

Query Match 62.9%; Score 70.5; DB 9; Length 37;
Best Local Similarity 62.5%; Pred. No. 3.5e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

Qy 4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
|| ||| ||||||| | |||||||
Db 4 GTFTSALSKQMEEEAVRLFIEWLKNGGXSSGA 35

RESULT 7
US-10-157-224A-99
; Sequence 99, Application US/10157224A
; Publication No. US20030087820A1
; GENERAL INFORMATION:
; APPLICANT: YOUNG, ANDREW A.
; APPLICANT: KOLTERMAN, ORVILLE G.
; TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
; TITLE OF INVENTION: ADMINISTRATION THEREOF
; FILE REFERENCE: 02001-050
; CURRENT APPLICATION NUMBER: US/10/157,224A
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: 09/889,330
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/00902
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/116,380
; PRIOR FILING DATE: 1999-01-14
; PRIOR APPLICATION NUMBER: 60/175,365
; PRIOR FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 188
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
; FEATURE:
; OTHER INFORMATION: c-term amidation
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (31)
; OTHER INFORMATION: Homoproline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (36)..(37)
; OTHER INFORMATION: Homoproline
US-10-157-224A-99

Query Match 62.9%; Score 70.5; DB 9; Length 37;
Best Local Similarity 62.5%; Pred. No. 3.5e-06;
Matches 20; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

Qy 4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
|| ||| ||||||| | |||||||
Db 4 GTFTSDASKQMEEEAVRLFIEWLKNGGXSSGA 35

RESULT 8
US-10-157-224A-183
; Sequence 183, Application US/10157224A
; Publication No. US20030087820A1
; GENERAL INFORMATION:
; APPLICANT: YOUNG, ANDREW A.
; APPLICANT: KOLTERMAN, ORVILLE G.
; TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
; TITLE OF INVENTION: ADMINISTRATION THEREOF
; FILE REFERENCE: 02001-050
; CURRENT APPLICATION NUMBER: US/10/157,224A
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: 09/889,330
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/00902
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/116,380
; PRIOR FILING DATE: 1999-01-14
; PRIOR APPLICATION NUMBER: 60/175,365
; PRIOR FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 188
; SOFTWARE: PatentIn Ver. 2.1

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;  TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
;  TITLE OF INVENTION:  ADMINISTRATION THEREOF
;  FILE REFERENCE: 02001-050
;  CURRENT APPLICATION NUMBER: US/10/157,224A
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: 09/889,330
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: PCT/US00/00902
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 60/116,380
;  PRIOR FILING DATE: 1999-01-14
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 171
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
;   FEATURE:
;   OTHER INFORMATION: c-term amidation
US-10-157-224A-171

  Query Match            62.9%;  Score 70.5;  DB 9;  Length 36;
  Best Local Similarity  59.4%;  Pred. No. 3.4e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| ||||||||    |  || ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 3
US-10-187-051-171
; Sequence 171, Application US/10187051
; Publication No. US20030087821A1
; GENERAL INFORMATION:
;  APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
;  APPLICANT:  PRICKETT, KATHRYN S.
;  APPLICANT:  BHAVSAR, SUNIL
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
;  TITLE OF INVENTION:  THE REDUCTION OF FOOD INTAKE
;  FILE REFERENCE: 231/181
;  CURRENT APPLICATION NUMBER: US/10/187,051
;  CURRENT FILING DATE:  2002-06-28
;  PRIOR APPLICATION NUMBER: US/09/003,869
;  PRIOR FILING DATE: 1998-01-07
;  PRIOR APPLICATION NUMBER: US 60/034,905
;  PRIOR FILING DATE: 1997-01-07
;  PRIOR APPLICATION NUMBER: US 60/055,404
;  PRIOR FILING DATE: 1997-08-08
;  PRIOR APPLICATION NUMBER: US 60/065,442
;  PRIOR FILING DATE: 1997-11-14
;  PRIOR APPLICATION NUMBER: US 60/066,029
;  PRIOR FILING DATE: 1997-11-14
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 171
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificially synthesized sequence of novel exendin
;   OTHER INFORMATION: agonist
;   OTHER INFORMATION: compound
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (36)...(36)
;   OTHER INFORMATION: amidated Pro (Prolinamide)
US-10-187-051-171

  Query Match            62.9%;  Score 70.5;  DB 9;  Length 36;
  Best Local Similarity  59.4%;  Pred. No. 3.4e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| ||||||||    |  || ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 4
US-09-003-869-171
; Sequence 171, Application US/09003869A
; Patent No. US20020137666A1
; GENERAL INFORMATION:
;  APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
;  APPLICANT: PRICKETT, KATHRYN S.
;  APPLICANT: BHAVSAR, SUNIL
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
;  TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
;  FILE REFERENCE: 231/181
;  CURRENT APPLICATION NUMBER: US/09/003,869A
;  CURRENT FILING DATE: 1998-01-07
;  EARLIER APPLICATION NUMBER: US 60/034,905
;  EARLIER FILING DATE: 1997-01-07
;  EARLIER APPLICATION NUMBER: US 60/055,404
;  EARLIER FILING DATE: 1997-08-08
;  EARLIER APPLICATION NUMBER: US 60/065,442
;  EARLIER FILING DATE: 1997-11-14
;  EARLIER APPLICATION NUMBER: US 60/066,029
;  EARLIER FILING DATE: 1997-11-14
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 171
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificially synthesized sequence of novel exendin agonist
;   OTHER INFORMATION: compound
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (36)...(36)
;   OTHER INFORMATION: amidated Pro (Prolinamide)
US-09-003-869-171

  Query Match            62.9%;  Score 70.5;  DB 10;  Length 36;
  Best Local Similarity  59.4%;  Pred. No. 3.4e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| ||||||||    |  || ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 5
US-09-756-690A-99
; Sequence 99, Application US/09756690A
; Publication No. US20030036504A1
; GENERAL INFORMATION:
;  APPLICANT: KOLTERMAN, ORVILLE G.
;  APPLICANT:  YOUNG, ANDREW A.
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF
;  TITLE OF INVENTION:  TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
;  FILE REFERENCE: 249/124
;  CURRENT APPLICATION NUMBER: US/09/756,690A
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: PatentIn Ver 2.1
; SEQ ID NO 99
;   LENGTH: 37
;   TYPE: PRT
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OM protein - protein search, using sw model

Run on: June 24, 2003, 23:07:45 ; Search time 30.5 Seconds
(without alignments)
141.911 Million cell updates/sec

Title: US-09-889-331A-48
Perfect score: 112
Sequence: 1 XXXGTXXXXXSKQXEEEAVRLXXXXLXGGXSSGAXXXXXX 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	70.5	62.9	36	9	US-09-756-690A-171	Sequence 171, App
2	70.5	62.9	36	9	US-10-157-224A-171	Sequence 171, App
3	70.5	62.9	36	9	US-10-187-051-171	Sequence 171, App
4	70.5	62.9	36	10	US-09-003-869-171	Sequence 171, App
5	70.5	62.9	37	9	US-09-756-690A-99	Sequence 99, Appl
6	70.5	62.9	37	9	US-09-756-690A-183	Sequence 183, App
7	70.5	62.9	37	9	US-10-157-224A-99	Sequence 99, Appl
8	70.5	62.9	37	9	US-10-157-224A-183	Sequence 183, App
9	70.5	62.9	37	9	US-10-187-051-99	Sequence 99, Appl
10	70.5	62.9	37	9	US-10-187-051-183	Sequence 183, App
11	70.5	62.9	37	10	US-09-003-869-99	Sequence 99, Appl
12	70.5	62.9	37	10	US-09-003-869-183	Sequence 183, App
13	70.5	62.9	39	9	US-09-756-690A-35	Sequence 35, Appl
14	70.5	62.9	39	9	US-09-756-690A-36	Sequence 36, Appl
15	70.5	62.9	39	9	US-09-756-690A-39	Sequence 39, Appl
16	70.5	62.9	39	9	US-10-157-224A-35	Sequence 35, Appl
17	70.5	62.9	39	9	US-10-157-224A-36	Sequence 36, Appl
18	70.5	62.9	39	9	US-10-157-224A-39	Sequence 39, Appl
19	70.5	62.9	39	9	US-10-187-051-35	Sequence 35, Appl
20	70.5	62.9	39	9	US-10-187-051-36	Sequence 36, Appl
21	70.5	62.9	39	9	US-10-187-051-39	Sequence 39, Appl
22	70.5	62.9	39	10	US-09-003-869-35	Sequence 35, Appl
23	70.5	62.9	39	10	US-09-003-869-36	Sequence 36, Appl
24	70.5	62.9	39	10	US-09-003-869-39	Sequence 39, Appl
25	70	62.5	38	9	US-09-756-690A-11	Sequence 11, Appl
26	69.5	62.1	35	9	US-09-756-690A-69	Sequence 69, Appl
27	69.5	62.1	35	9	US-09-756-690A-173	Sequence 173, App
28	69.5	62.1	35	9	US-10-157-224A-69	Sequence 69, Appl
29	69.5	62.1	35	9	US-10-157-224A-173	Sequence 173, App
30	69.5	62.1	35	9	US-10-187-051-69	Sequence 69, Appl
31	69.5	62.1	35	9	US-10-187-051-173	Sequence 173, App
32	69.5	62.1	35	10	US-09-003-869-69	Sequence 69, Appl
33	69.5	62.1	35	10	US-09-003-869-173	Sequence 173, App
34	69.5	62.1	36	9	US-09-756-690A-67	Sequence 67, Appl
35	69.5	62.1	36	9	US-09-756-690A-86	Sequence 86, Appl
36	69.5	62.1	36	9	US-09-756-690A-170	Sequence 170, App
37	69.5	62.1	36	9	US-09-756-690A-184	Sequence 184, App
38	69.5	62.1	36	9	US-10-157-224A-67	Sequence 67, Appl
39	69.5	62.1	36	9	US-10-157-224A-86	Sequence 86, Appl
40	69.5	62.1	36	9	US-10-157-224A-170	Sequence 170, App
41	69.5	62.1	36	9	US-10-157-224A-184	Sequence 184, App
42	69.5	62.1	36	9	US-10-187-051-67	Sequence 67, Appl
43	69.5	62.1	36	9	US-10-187-051-86	Sequence 86, Appl
44	69.5	62.1	36	9	US-10-187-051-170	Sequence 170, App
45	69.5	62.1	36	9	US-10-187-051-184	Sequence 184, App

ALIGNMENTS

RESULT 1
US-09-756-690A-171
; Sequence 171, Application US/09756690A
; Publication No. US20030036504A1
; GENERAL INFORMATION:
; APPLICANT: KOLTERMAN, ORVILLE G.
; APPLICANT: YOUNG, ANDREW A.
; TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF
; TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
; FILE REFERENCE: 249/124
; CURRENT APPLICATION NUMBER: US/09/756,690A
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/175,365
; PRIOR FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 188
; SOFTWARE: PatentIn Ver 2.1
; SEQ ID NO 171
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
; FEATURE:
; OTHER INFORMATION: c-term amidation
US-09-756-690A-171

Query Match 62.9%; Score 70.5; DB 9; Length 36;
Best Local Similarity 59.4%; Pred. No. 3.4e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

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Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35
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RESULT 2
US-10-157-224A-171
; Sequence 171, Application US/10157224A
; Publication No. US20030087820A1
; GENERAL INFORMATION:
; APPLICANT: YOUNG, ANDREW A.
; APPLICANT: KOLTERMAN, ORVILLE G.

Search completed: June 24, 2003, 23:05:18
Job time : 49.5 secs

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PS   Claim 18; Fig 4; 108pp; English.
XX
CC   AAY24809 to AAY24877 represent exendin agonist peptides which can
CC   regulate gastric motility and slow gastric emptying. The peptides can be
CC   used for treating e.g. diabetes or hyperglycaemic or hypoglycaemic
CC   conditions. The peptides are exendin agonists which have activity as
CC   agents to regulate gastric motility and to slow gastric emptying, as
CC   evidenced by the ability to reduce post-prandial glucose levels in
CC   mammals. They can be used for the treatment of Type I and II diabetes and
CC   hyperglycaemic or hypoglycaemic conditions. They can also be used for the
CC   treatment of disorders which would be benefited by agents which lower
CC   plasma glucose levels and in treatment of disorders which would be
CC   benefited with agents useful in delaying and/or slowing gastric
CC   emptying.
XX
SQ   Sequence   37 AA;

  Query Match             62.9%;  Score 70.5;  DB 20;  Length 37;
  Best Local Similarity   62.5%;  Pred. No. 2.8e-06;
  Matches   20;  Conservative    0;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  |||||||
Db          4 GTFTSDASKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 14
AAY24853
ID   AAY24853 standard; peptide; 37 AA.
XX
AC   AAY24853;
XX
DT   24-AUG-1999  (first entry)
XX
DE   Exendin agonist peptide #45.
XX
KW   Exendin; agonist; Heloderma sp.; Gila monster; venom; lizard;
KW   diabetes mellitus type I; diabetes mellitus type II; hyperglycaemia;
KW   hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.
XX
OS   Synthetic.
OS   Heloderma sp.
XX
PN   WO9925727-A2.
XX
PD   27-MAY-1999.
XX
PF   13-NOV-1998;   98WO-US24210.
XX
PR   14-NOV-1997;   97US-0065442.
XX
PA   (AMYL-) AMYLIN PHARM INC.
XX
PI   Beeley NRA,  Prickett KS;
XX
DR   WPI; 1999-394773/33.
XX
PT   New exendin agonist peptides  - can regulate gastric motility and
PT   slow gastric emptying, used for treating, e.g. diabetes
XX
PS   Claim 18; Fig 4; 108pp; English.
XX
CC   AAY24809 to AAY24877 represent exendin agonist peptides which can
CC   regulate gastric motility and slow gastric emptying. The peptides can be
CC   used for treating e.g. diabetes or hyperglycaemic or hypoglycaemic
CC   conditions. The peptides are exendin agonists which have activity as
CC   agents to regulate gastric motility and to slow gastric emptying, as
CC   evidenced by the ability to reduce post-prandial glucose levels in
CC   mammals. They can be used for the treatment of Type I and II diabetes and
CC   hyperglycaemic or hypoglycaemic conditions. They can also be used for the
CC   treatment of disorders which would be benefited by agents which lower
CC   plasma glucose levels and in treatment of disorders which would be
CC   benefited with agents useful in delaying and/or slowing gastric
CC   emptying.
XX
SQ   Sequence   37 AA;

  Query Match             62.9%;  Score 70.5;  DB 20;  Length 37;
  Best Local Similarity   59.4%;  Pred. No. 2.8e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  |||||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGASSGA 35


RESULT 15
AAY24854
ID   AAY24854 standard; peptide; 37 AA.
XX
AC   AAY24854;
XX
DT   24-AUG-1999  (first entry)
XX
DE   Exendin agonist peptide #46.
XX
KW   Exendin; agonist; Heloderma sp.; Gila monster; venom; lizard;
KW   diabetes mellitus type I; diabetes mellitus type II; hyperglycaemia;
KW   hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.
XX
OS   Synthetic.
OS   Heloderma sp.
XX
PN   WO9925727-A2.
XX
PD   27-MAY-1999.
XX
PF   13-NOV-1998;   98WO-US24210.
XX
PR   14-NOV-1997;   97US-0065442.
XX
PA   (AMYL-) AMYLIN PHARM INC.
XX
PI   Beeley NRA,  Prickett KS;
XX
DR   WPI; 1999-394773/33.
XX
PT   New exendin agonist peptides  - can regulate gastric motility and
PT   slow gastric emptying, used for treating, e.g. diabetes
XX
PS   Claim 18; Fig 4; 108pp; English.
XX
CC   AAY24809 to AAY24877 represent exendin agonist peptides which can
CC   regulate gastric motility and slow gastric emptying. The peptides can be
CC   used for treating e.g. diabetes or hyperglycaemic or hypoglycaemic
CC   conditions. The peptides are exendin agonists which have activity as
CC   agents to regulate gastric motility and to slow gastric emptying, as
CC   evidenced by the ability to reduce post-prandial glucose levels in
CC   mammals. They can be used for the treatment of Type I and II diabetes and
CC   hyperglycaemic or hypoglycaemic conditions. They can also be used for the
CC   treatment of disorders which would be benefited by agents which lower
CC   plasma glucose levels and in treatment of disorders which would be
CC   benefited with agents useful in delaying and/or slowing gastric
CC   emptying.
XX
SQ   Sequence   37 AA;

  Query Match             62.9%;  Score 70.5;  DB 20;  Length 37;
  Best Local Similarity   59.4%;  Pred. No. 2.8e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  |||||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGASSGA 35
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XX
PD 19-JUL-2001.
XX
PF 09-JAN-2001; 2001WO-US00719.
XX
PR 10-JAN-2000; 2000US-0175365.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Kolterman OG, Young AA;
XX
DR WPI; 2001-514422/56.
XX
PT Use of exendin and exendin agonist compounds for modulating
PT triglyceride levels, and treating heart disease and dyslipidemia -
XX
PS Example 166; Page 136; 161pp; English.
XX
CC The patent discloses a method for modulating plasma or postprandial
CC triglyceride and other lipid levels by administering exendin or an
CC exendin agonist. Exendins have inotropic and diuretic effects. They
CC suppress the secretion of glucagon. Exendin and its agonists have
CC a significant effect on the reduction of blood serum triglyceride
CC concentrations. They are used to treat coronary heart disease and
CC dyslipidaemia, and for modifying postprandial triglyceride levels.
CC The present peptide sequence is an agonist of exendin.
XX
SQ Sequence 36 AA;

Query Match 62.9%; Score 70.5; DB 22; Length 36;
Best Local Similarity 59.4%; Pred. No. 2.7e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
|| ||| ||||||| | || ||||
Db 4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35

RESULT 12
AAB64351
ID AAB64351 standard; peptide; 36 AA.
XX
AC AAB64351;
XX
DT 27-MAR-2001 (first entry)
XX
DE Exendin agonist, SEQ ID NO:171.
XX
KW Exendin agonist; gestational diabetes mellitus; GDM; insulin resistance;
KW pregnancy complication; neonatal abnormality; blood glucose modulator;
KW insulinotropic; anorectic; exendin-4.
XX
OS Heloderma suspectum.
OS Synthetic.
XX
PN WO200073331-A2.
XX
PD 07-DEC-2000.
XX
PF 23-MAY-2000; 2000WO-US14231.
XX
PR 01-JUN-1999; 99US-0323867.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Hiles R, Prickett KS;
XX
DR WPI; 2001-137634/14.
XX
PT Use of exendins or exendin agonists for lowering or reducing blood
PT glucose levels and treating gestational diabetes mellitus in a subject,
PT especially in a human -
XX
PS Example 166; Page 113; 133pp; English.
XX
CC The invention relates to the use of an exendin (AAB64181-B64182) or
CC an exendin agonist (AAB64185-B64368) for treating gestational diabetes
CC mellitus (GDM) in a patient. GDM arises during pregnancy, and is due
CC to a combination of increased insulin resistance and a diminished
CC ability to increase insulin secretion. In contrast, in a normal
CC pregnancy, both insulin resistance and insulin secretion increase. GDM
CC pregnancies are associated with complications in both the mother and the
CC foetus. Women with GDM have increased rates of Caesarian delivery,
CC hypertensive disorders such as pre-eclampsia, and urinary tract
CC infections. GDM results in an elevated rate of foetal abnormalities such
CC as neural tube defects, and is associated with an increased risk of
CC neonatal morbidites such as hypoglycaemia, hypocalcaemia,
CC hypomagnesaemia, polycythaemia, hyperbilirubinaemia, and subsequent
CC childhood and adolescent obesity. Exendins are peptides from the salivary
CC secretions of the Gila monster (exendin-4) and the Mexican beaded lizard
CC (exendin-3) which exhibit homology with several members of the
CC glucagon-like peptide family, particularly GLP-1, and have similar
CC insulinotropic effects. Unlike the compounds used to treat type 2
CC diabetes, which are contraindicated for GDM, exendins and exendin
CC agonists do not cross the placenta and thus do not cause severe prolonged
CC hypoglycaemia in the newborn. They have a potent and prolonged effect on
CC blood glucose, and, unlike conventional insulin therapy, should not cause
CC weight gain, as they inhibit gastric emptying and reduce appetite. The
CC present sequence represents a exendin agonist of the invention which is
CC based upon the sequence of exendin-4.
XX
SQ Sequence 36 AA;

Query Match 62.9%; Score 70.5; DB 22; Length 36;
Best Local Similarity 59.4%; Pred. No. 2.7e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
|| ||| ||||||| | || ||||
Db 4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35

RESULT 13
AAY24869
ID AAY24869 standard; peptide; 37 AA.
XX
AC AAY24869;
XX
DT 24-AUG-1999 (first entry)
XX
DE Exendin agonist peptide #61.
XX
KW Exendin; agonist; Heloderma sp.; Gila monster; venom; lizard;
KW diabetes mellitus type I; diabetes mellitus type II; hyperglycaemia;
KW hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.
XX
OS Synthetic.
OS Heloderma sp.
XX
PN WO9925727-A2.
XX
PD 27-MAY-1999.
XX
PF 13-NOV-1998; 98WO-US24210.
XX
PR 14-NOV-1997; 97US-0065442.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Beeley NRA, Prickett KS;
XX
DR WPI; 1999-394773/33.
XX
PT New exendin agonist peptides - can regulate gastric motility and
PT slow gastric emptying, used for treating, e.g. diabetes
XX

```
Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| ||||||| |  || ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35
```

RESULT 9
AAB53029
ID AAB53029 standard; Peptide; 36 AA.
XX
AC AAB53029;
XX
DT 28-FEB-2001 (first entry)
XX
DE Extendin agonist compound #157.
XX
KW Extendin; agonist; diabetes; obesity; eating disorder;
KW dyslipidaemia; insulin-resistance syndrome; food intake.
XX
OS Heloderma sp.
XX
PN WO200066629-A1.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US11814.
XX
PR 30-APR-1999; 99US-0132018.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Young A, Prickett K;
XX
DR WPI; 2000-672834/65.
XX
PT Modified exendin or an exendin agonist linked to one or more
PT polyethylene glycol (PEG) polymers, modulate plasma glucose levels,
PT useful for treating disorders such as diabetes and obesity -
XX
PS Disclosure; Fig 4; 119pp; English.
XX
CC The present invention relates to extendins and their agonists which have
CC been modified with molecular weight increasing agents such as
CC polyethylene glycol (PEG). These can be used in the treatment of
CC diabetes, obesity, impaired glucose tolerance, postprandial dumping
CC syndrome, postprandial hyperglycaemia, eating disorders, insulin
CC resistance syndrome, dyslipidaemia and to suppress glucagon secretion.
XX
SQ Sequence 36 AA;

Query Match 62.9%; Score 70.5; DB 21; Length 36;
Best Local Similarity 59.4%; Pred. No. 2.7e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

```
Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| ||||||| |  || ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35
```

RESULT 10
AAY94184
ID AAY94184 standard; peptide; 36 AA.
XX
AC AAY94184;
XX
DT 20-OCT-2000 (first entry)
XX
DE Amino acid sequence of an extendin agonist.
XX
KW Extendin; Gila monster lizard; Mexican Beaded lizard; agonist;
KW glucagon-like peptide; plasma glucagon; necrolytic erythema;
KW glucagonoma; hyperglucagonemia; diabetes.
XX
OS Synthetic.
OS Heloderma sp.
XX
FH Key Location/Qualifiers
FT Modified-site 36
FT /note= "amidated residue"
XX
PN WO200041548-A2.
XX
PD 20-JUL-2000.
XX
PF 14-JAN-2000; 2000WO-US00942.
XX
PR 14-JAN-1999; 99US-0116380.
PR 30-APR-1999; 99US-0132017.
PR 10-JAN-2000; 2000US-0175365.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Young A, Gedulin B;
XX
DR WPI; 2000-490999/43.
XX
PT Lowering plasma glucagon using exendin, an exendin agonist, a modified
PT exendin or a modified exendin agonist, useful for treating
PT hyperglucagonemia and diabetes -
XX
PS Disclosure; Fig 4G; 96pp; English.
XX
CC The present sequence represents a modified extendin or extendin agonist.
CC Extendins are found in the salivary glands of the Gila monster and
CC Mexican Beaded lizard, and have sequence similarity to glucagon-like
CC peptides. They are used in the method of the invention. The specification
CC describes a method for lowering plasma glucagon, comprising administering
CC an exendin, an exendin agonist, a modified exendin or a modified exendin
CC agonist. These compounds lower plasma glucagon level. The method is
CC useful for lowering plasma glucagon in subjects, preferably humans,
CC suffering from necrolytic erythema or glucagonoma. The method is also
CC useful for treating hyperglucagonemia and other conditions that would
CC benefit from reduced glucagon levels and/or suppression of glucagon,
CC e.g. type 1 and type 2 diabetes.
XX
SQ Sequence 36 AA;

Query Match 62.9%; Score 70.5; DB 21; Length 36;
Best Local Similarity 59.4%; Pred. No. 2.7e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

```
Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| ||||||| |  || ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35
```

RESULT 11
AAE08515
ID AAE08515 standard; peptide; 36 AA.
XX
AC AAE08515;
XX
DT 01-NOV-2001 (first entry)
XX
DE Exendin agonist peptide #160.
XX
KW Exendin agonist; antilipemic; cardiant; triglyceride; inotropic;
KW diuretic; coronary heart disease; dyslipidaemia.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 36
FT /note= "C-terminal amide"
XX
PN WO200151078-A1.

XX
PN WO200151078-A1.
XX
PD 19-JUL-2001.
XX
PF 09-JAN-2001; 2001WO-US00719.
XX
PR 10-JAN-2000; 2000US-0175365.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Kolterman OG, Young AA;
XX
DR WPI; 2001-514422/56.
XX
PT Use of exendin and exendin agonist compounds for modulating
PT triglyceride levels, and treating heart disease and dyslipidemia -
XX
PS Example 30; Page -; 161pp; English.
XX
CC The patent discloses a method for modulating plasma or postprandial
CC triglyceride and other lipid levels by administering exendin or an
CC exendin agonist. Exendins have inotropic and diuretic effects. They
CC suppress the secretion of glucagon. Exendin and its agonists have
CC a significant effect on the reduction of blood serum triglyceride
CC concentrations. They are used to treat coronary heart disease and
CC dyslipidaemia, and for modifying postprandial triglyceride levels.
CC The present peptide sequence is an agonist of exendin.
CC Note: The present sequence is not shown in the specification but is
CC derived from SEQ ID NO:3 shown in page 17 of the specification.
XX
SQ Sequence 39 AA;

Query Match 63.8%; Score 71.5; DB 22; Length 39;
Best Local Similarity 59.4%; Pred. No. 1.9e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
|| ||| ||||||| | || ||||
Db 4 GTFTSDLSKQLEEEAVRLFIEFLKNGGASSGA 35

RESULT 7
AAY17606
ID AAY17606 standard; peptide; 36 AA.
XX
AC AAY17606;
XX
DT 09-AUG-1999 (first entry)
XX
DE Exendin agonist peptide #72.
XX
KW Exendin; agonist; Heloderma sp.; Gila monster; venom; lizard;
KW diabetes mellitus type I; diabetes mellitus type II; hyperglycaemia;
KW hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.
XX
OS Synthetic.
OS Heloderma sp.
XX
PN WO9925728-A1.
XX
PD 27-MAY-1999.
XX
PF 13-NOV-1998; 98WO-US24273.
XX
PR 14-NOV-1997; 97US-0066029.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Beeley NRA, Prickett KS;
XX
DR WPI; 1999-347456/29.
XX
PT Peptide agonists of exendin - delay stomach emptying, for treating
PT diabetes and hypo- or hyper-glycaemia
XX
PS Claim 28; Fig 4; 144pp; English.
XX
CC AAY17535 to AAY17624 represent exendin peptide agonists. Exendins are
CC peptides that are found in the venom of the Gila-monster, a lizard
CC endogenous to Arizona and Northern Mexico. The peptide agonists are
CC used to treat diabetes mellitus (types I or II), hyperglycaemia or
CC hypoglycaemia. They can also be used for in vitro and in vivo studies
CC on exendins and their agonists. They regulate gastric motility and slow
CC gastric emptying (resulting in lower post-prandial glucose levels).
XX
SQ Sequence 36 AA;

Query Match 62.9%; Score 70.5; DB 20; Length 36;
Best Local Similarity 59.4%; Pred. No. 2.7e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
|| ||| ||||||| | || ||||
Db 4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35

RESULT 8
AAB11263
ID AAB11263 standard; Peptide; 36 AA.
XX
AC AAB11263;
XX
DT 20-FEB-2001 (first entry)
XX
DE exendin agonist peptide SEQ ID NO 171.
XX
KW Exendin; agonist; treatment; antidiabetic; insulin sensitivity; diabetes;
KW plasma glucose; gastric emptying; food intake.
XX
OS Synthetic.
XX
PN WO200041546-A2.
XX
PD 20-JUL-2000.
XX
PF 10-JAN-2000; 2000US-0116380.
XX
PR 14-JAN-1999; 99US-0116380.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Young A, L'Italien JJ, Kolterman O;
XX
DR WPI; 2000-514584/46.
XX
PT New formulations comprising an exendin or exendin agonist peptide used
PT for increasing the sensitivity of a subject to insulin to treat
PT diabetes -
XX
PS Example 180; Page 229; 281pp; English.
XX
CC This invention describes a novel formulation (I) comprising an exendin or
CC exendin agonist peptide, a buffer and an iso-osmolality modifier which
CC has a pH of 3-7. The products of the invention have antidiabetic
CC activity. The exendin or exendin agonist is used to increase the
CC sensitivity of a subject to insulin to treat diabetes and disorders which
CC would benefit from agents which lower plasma glucose levels and disorders
CC which would benefit from agents that delay and/or slow gastric emptying
CC or reducing food intake.
XX
SQ Sequence 36 AA;

Query Match 62.9%; Score 70.5; DB 21; Length 36;
Best Local Similarity 59.4%; Pred. No. 2.7e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

XX
KW Exendin agonist; gestational diabetes mellitus; GDM; insulin resistance;
KW pregnancy complication; neonatal abnormality; blood glucose modulator;
KW insulinotropic; anorectic; exendin-4.
XX
OS Heloderma suspectum.
OS Synthetic.
XX
PN WO200073331-A2.
XX
PD 07-DEC-2000.
XX
PF 23-MAY-2000; 2000WO-US14231.
XX
PR 01-JUN-1999; 99US-0323867.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Hiles R, Prickett KS;
XX
DR WPI; 2001-137634/14.
XX
PT Use of exendins or exendin agonists for lowering or reducing blood
PT glucose levels and treating gestational diabetes mellitus in a subject,
PT especially in a human -
XX
PS Example 178; Page 119; 133pp; English.
XX
CC The invention relates to the use of an exendin (AAB64181-B64182) or
CC an exendin agonist (AAB64185-B64368) for treating gestational diabetes
CC mellitus (GDM) in a patient. GDM arises during pregnancy, and is due
CC to a combination of increased insulin resistance and a diminished
CC ability to increase insulin secretion. In contrast, in a normal
CC pregnancy, both insulin resistance and insulin secretion increase. GDM
CC pregnancies are associated with complications in both the mother and the
CC foetus. Women with GDM have increased rates of Caesarian delivery,
CC hypertensive disorders such as pre-eclampsia, and urinary tract
CC infections. GDM results in an elevated rate of foetal abnormalities such
CC as neural tube defects, and is associated with an increased risk of
CC neonatal morbidites such as hypoglycaemia, hypocalcaemia,
CC hypomagnesaemia, polycythaemia, hyperbilirubinaemia, and subsequent
CC childhood and adolescent obesity. Exendins are peptides from the salivary
CC secretions of the Gila monster (exendin-4) and the Mexican beaded lizard
CC (exendin-3) which exhibit homology with several members of the
CC glucagon-like peptide family, particularly GLP-1, and have similar
CC insulinotropic effects. Unlike the compounds used to treat type 2
CC diabetes, which are contraindicated for GDM, exendins and exendin
CC agonists do not cross the placenta and thus do not cause severe prolonged
CC hypoglycaemia in the newborn. They have a potent and prolonged effect on
CC blood glucose, and, unlike conventional insulin therapy, should not cause
CC weight gain, as they inhibit gastric emptying and reduce appetite. The
CC present sequence represents a exendin agonist of the invention which is
CC based upon the sequence of exendin-4.
XX
SQ Sequence 37 AA;

Query Match 63.8%; Score 71.5; DB 22; Length 37;
Best Local Similarity 59.4%; Pred. No. 1.8e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
|| ||| ||||||| | || ||||
Db 4 GTFTSALSKQMEEEAVRLFIEWLKNGGASSGA 35

RESULT 5
AAB11313
ID AAB11313 standard; Peptide; 39 AA.
XX
AC AAB11313;
XX
DT 20-FEB-2001 (first entry)
XX
DE exendin agonist peptide SEQ ID NO 39.
XX
KW Exendin; agonist; treatment; antidiabetic; insulin sensitivity; diabetes;
KW plasma glucose; gastric emptying; food intake.
XX
OS Synthetic.
XX
PN WO200041546-A2.
XX
PD 20-JUL-2000.
XX
PF 10-JAN-2000; 2000US-0116380.
XX
PR 14-JAN-1999; 99US-0116380.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Young A, L'Italien JJ, Kolterman O;
XX
DR WPI; 2000-514584/46.
XX
PT New formulations comprising an exendin or exendin agonist peptide used
PT for increasing the sensitivity of a subject to insulin to treat
PT diabetes -
XX
PS Example 44; Figure 15; 281pp; English.
XX
CC This invention describes a novel formulation (I) comprising an exendin or
CC exendin agonist peptide, a buffer and an iso-osmolality modifier which
CC has a pH of 3-7. The products of the invention have antidiabetic
CC activity. The exendin or exendin agonist is used to increase the
CC sensitivity of a subject to insulin to treat diabetes and disorders which
CC would benefit from agents which lower plasma glucose levels and disorders
CC which would benefit from agents that delay and/or slow gastric emptying
CC or reducing food intake.
XX
SQ Sequence 39 AA;

Query Match 63.8%; Score 71.5; DB 21; Length 39;
Best Local Similarity 59.4%; Pred. No. 1.9e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
|| ||| ||||||| | || ||||
Db 4 GTFTSDLSKQLEEEAVRLFIEFLKNGGASSGA 35

RESULT 6
AAE08383
ID AAE08383 standard; peptide; 39 AA.
XX
AC AAE08383;
XX
DT 01-NOV-2001 (first entry)
XX
DE Exendin agonist peptide #30.
XX
KW Exendin agonist; antilipemic; cardiant; triglyceride; inotropic;
KW diuretic; coronary heart disease; dyslipidaemia.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 31
FT /note= "N-Methyl-alanine"
FT Modified-site 36
FT /note= "N-Methyl-alanine"
FT Modified-site 37
FT /note= "N-Methyl-alanine"
FT Modified-site 38
FT /note= "N-Methyl-alanine"
FT Modified-site 39
FT /note= "C-terminal amide"

```
PS   Disclosure; Page 52-53; 119pp; English.
XX
CC   The present invention relates to extendins and their agonists which have
CC   been modified with molecular weight increasing agents such as
CC   polyethylene glycol (PEG). These can be used in the treatment of
CC   diabetes, obesity, impaired glucose tolerance, postprandial dumping
CC   syndrome, postprandial hyperglycaemia, eating disorders, insulin
CC   resistance syndrome, dyslipidaemia and to suppress glucagon secretion.
XX
SQ   Sequence   38 AA;

  Query Match             70.5%;  Score 79;  DB 21;  Length 38;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-08;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLXGGXSSGA 34
              |||||||||||||||||||||||||||||||
Db          4 GTXXXXXSKQXEEEAVRLXXXXLXGGXSSGA 34


RESULT 2
AAY17618
ID   AAY17618 standard; peptide; 37 AA.
XX
AC   AAY17618;
XX
DT   09-AUG-1999  (first entry)
XX
DE   Exendin agonist peptide #84.
XX
KW   Exendin; agonist; Heloderma sp.; Gila monster; venom; lizard;
KW   diabetes mellitus type I; diabetes mellitus type II; hyperglycaemia;
KW   hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.
XX
OS   Synthetic.
OS   Heloderma sp.
XX
PN   WO9925728-A1.
XX
PD   27-MAY-1999.
XX
PF   13-NOV-1998;   98WO-US24273.
XX
PR   14-NOV-1997;   97US-0066029.
XX
PA   (AMYL-) AMYLIN PHARM INC.
XX
PI   Beeley NRA,  Prickett KS;
XX
DR   WPI; 1999-347456/29.
XX
PT   Peptide agonists of exendin - delay stomach emptying, for treating
PT   diabetes and hypo- or hyper-glycaemia
XX
PS   Claim 28; Fig 4; 144pp; English.
XX
CC   AAY17535 to AAY17624 represent exendin peptide agonists. Exendins are
CC   peptides that are found in the venom of the Gila-monstar, a lizard
CC   endogenous to Arizona and Northern Mexico. The peptide agonists are
CC   used to treat diabetes mellitus (types I or II), hyperglycaemia or
CC   hypoglycaemia. They can also be used for in vitro and in vivo studies
CC   on exendins and their agonists. They regulate gastric motility and slow
CC   gastric emptying (resulting in lower post-prandial glucose levels).
XX
SQ   Sequence   37 AA;

  Query Match             63.8%;  Score 71.5;  DB 20;  Length 37;
  Best Local Similarity   59.4%;  Pred. No. 1.8e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSALSKQMEEEAVRLFIEWLKNGGASSGA 35


RESULT 3
AAE08527
ID   AAE08527 standard; peptide; 37 AA.
XX
AC   AAE08527;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Exendin agonist peptide #172.
XX
KW   Exendin agonist; antilipemic; cardiant; triglyceride; inotropic;
KW   diuretic; coronary heart disease; dyslipidaemia.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   31
FT                   /note= "N-methyl alanine"
FT   Modified-site   36
FT                   /note= "N-methyl alanine"
FT   Modified-site   37
FT                   /note= "N-methyl alanine; C-terminal amide"
XX
PN   WO200151078-A1.
XX
PD   19-JUL-2001.
XX
PF   09-JAN-2001; 2001WO-US00719.
XX
PR   10-JAN-2000; 2000US-0175365.
XX
PA   (AMYL-) AMYLIN PHARM INC.
XX
PI   Kolterman OG,  Young AA;
XX
DR   WPI; 2001-514422/56.
XX
PT   Use of exendin and exendin agonist compounds for modulating
PT   triglyceride levels, and treating heart disease and dyslipidemia -
XX
PS   Example 178; Page 143; 161pp; English.
XX
CC   The patent discloses a method for modulating plasma or postprandial
CC   triglyceride and other lipid levels by administering exendin or an
CC   exendin agonist. Exendins have inotropic and diuretic effects. They
CC   suppress the secretion of glucagon. Exendin and its agonists have
CC   a significant effect on the reduction of blood serum triglyceride
CC   concentrations. They are used to treat coronary heart disease and
CC   dyslipidaemia, and for modifying postprandial triglyceride levels.
CC   The present peptide sequence is an agonist of exendin.
XX
SQ   Sequence   37 AA;

  Query Match             63.8%;  Score 71.5;  DB 22;  Length 37;
  Best Local Similarity   59.4%;  Pred. No. 1.8e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSALSKQMEEEAVRLFIEWLKNGGASSGA 35


RESULT 4
AAB64363
ID   AAB64363 standard; peptide; 37 AA.
XX
AC   AAB64363;
XX
DT   27-MAR-2001  (first entry)
XX
DE   Exendin agonist, SEQ ID NO:183.
```

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OM protein - protein search, using sw model

Run on: June 24, 2003, 22:59:19 ; Search time 49.5 Seconds
(without alignments)
107.677 Million cell updates/sec

Title: US-09-889-331A-48
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	79	70.5	38	21	AAB52839	Extendin agonist p
2	71.5	63.8	37	20	AAY17618	Exendin agonist pe
3	71.5	63.8	37	22	AAE08527	Exendin agonist pe
4	71.5	63.8	37	22	AAB64363	Exendin agonist, S
5	71.5	63.8	39	21	AAB11313	exendin agonist pe
6	71.5	63.8	39	22	AAE08383	Exendin agonist pe
7	70.5	62.9	36	20	AAY17606	Exendin agonist pe
8	70.5	62.9	36	21	AAB11263	exendin agonist pe
9	70.5	62.9	36	21	AAB53029	Extendin agonist c
10	70.5	62.9	36	21	AAY94184	Amino acid sequenc
11	70.5	62.9	36	22	AAE08515	Exendin agonist pe
12	70.5	62.9	36	22	AAB64351	Exendin agonist, S
13	70.5	62.9	37	20	AAY24869	Exendin agonist pe
14	70.5	62.9	37	20	AAY24853	Exendin agonist pe
15	70.5	62.9	37	20	AAY24854	Exendin agonist pe
16	70.5	62.9	37	21	AAB11275	exendin agonist pe
17	70.5	62.9	37	21	AAB53041	Extendin agonist c
18	70.5	62.9	37	21	AAY94196	Amino acid sequenc
19	70.5	62.9	37	22	AAE08427	Exendin agonist pe
20	70.5	62.9	37	22	AAE08428	Exendin agonist pe
21	70.5	62.9	37	22	AAE08443	Exendin agonist pe
22	70.5	62.9	37	22	AAB64263	Exendin agonist, S
23	70.5	62.9	37	22	AAB64264	Exendin agonist, S
24	70.5	62.9	37	22	AAB64279	Exendin agonist, S
25	70.5	62.9	39	21	AAB11311	exendin agonist pe
26	70.5	62.9	39	21	AAY94039	Amino acid sequenc
27	70.5	62.9	39	21	AAY94040	Amino acid sequenc
28	70.5	62.9	39	21	AAY94043	Amino acid sequenc
29	70.5	62.9	39	22	AAE08379	Exendin agonist pe
30	70.5	62.9	39	22	AAE08380	Exendin agonist pe
31	70.5	62.9	39	22	AAE08381	Exendin agonist pe
32	70.5	62.9	39	22	AAB64219	Exendin agonist, S
33	69.5	62.1	35	20	AAY31535	Exendin agonist pe
34	69.5	62.1	35	20	AAY24839	Exendin agonist pe
35	69.5	62.1	35	20	AAY17608	Exendin agonist pe
36	69.5	62.1	35	21	AAB11161	exendin agonist pe
37	69.5	62.1	35	21	AAB11265	exendin agonist pe
38	69.5	62.1	35	21	AAB52920	Extendin agonist c
39	69.5	62.1	35	21	AAB53031	Extendin agonist c
40	69.5	62.1	35	21	AAY94074	Amino acid sequenc
41	69.5	62.1	35	21	AAY94186	Amino acid sequenc
42	69.5	62.1	35	22	AAE08413	Exendin agonist pe
43	69.5	62.1	35	22	AAE08517	Exendin agonist pe
44	69.5	62.1	35	22	AAB64249	Exendin agonist, S
45	69.5	62.1	35	22	AAB64353	Exendin agonist, S

ALIGNMENTS

RESULT 1
AAB52839
ID AAB52839 standard; Peptide; 38 AA.
XX
AC AAB52839;
XX
DT 28-FEB-2001 (first entry)
XX
DE Extendin agonist peptide #9.
XX
KW Extendin; agonist; diabetes; obesity; eating disorder;
KW dyslipidaemia; insulin-resistance syndrome; food intake.
XX
OS Heloderma sp.
XX
PN WO200066629-A1.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US11814.
XX
PR 30-APR-1999; 99US-0132018.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Young A, Prickett K;
XX
DR WPI; 2000-672834/65.
XX
PT Modified exendin or an exendin agonist linked to one or more
PT polyethylene glycol (PEG) polymers, modulate plasma glucose levels,
PT useful for treating disorders such as diabetes and obesity -
XX

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RL   Nature 409:529-533(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / RIMD 0509952;
RX   MEDLINE=21156231; PubMed=11258796;
RA   Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA   Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA   Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA   Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT   "Complete genome sequence of enterohemorrhagic Escherichia coli
RT   O157:H7 and genomic comparison with a laboratory strain K-12.";
RL   DNA Res. 8:11-22(2001).
DR   EMBL; AE005466; AAG57475.1; -.
DR   EMBL; AP002561; BAB36653.1; -.
KW   Complete proteome.
SQ   SEQUENCE   310 AA;  34482 MW;  407D21FFF665D690 CRC64;

  Query Match             33.9%;  Score 38;  DB 16;  Length 310;
  Best Local Similarity   34.8%;  Pred. No. 35;
  Matches    8;  Conservative    4;  Mismatches   11;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLXGGXSSGA 34
              |: | :|: |    :  | | ||
Db         50 KELERDAMALLWSAIAAGLSMGA 72


RESULT 14
Q8ZNA4
ID   Q8ZNA4      PRELIMINARY;      PRT;   313 AA.
AC   Q8ZNA4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Putative transport.
GN   YFDC OR STM2393.
OS   Salmonella typhimurium.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Salmonella.
OX   NCBI_TaxID=602;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX   MEDLINE=21534948; PubMed=11677609;
RA   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA   Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA   Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA   Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA   Waterston R., Wilson R.K.;
RT   "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT   LT2.";
RL   Nature 413:852-856(2001).
DR   EMBL; AE008807; AAL21294.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   313 AA;  34917 MW;  430A474E07B640AC CRC64;

  Query Match             33.9%;  Score 38;  DB 16;  Length 313;
  Best Local Similarity   34.8%;  Pred. No. 36;
  Matches    8;  Conservative    4;  Mismatches   11;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLXGGXSSGA 34
              |: | :|: |    :  | | ||
Db         53 KEMERDAMALLWSAIAAGLSMGA 75


RESULT 15
Q8Z4Y7
ID   Q8Z4Y7      PRELIMINARY;      PRT;   313 AA.
AC   Q8Z4Y7;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Putative membrane protein.
GN   STY2625.
OS   Salmonella typhi.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Salmonella.
OX   NCBI_TaxID=601;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CT18;
RX   MEDLINE=21534947; PubMed=11677608;
RA   Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA   Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA   Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA   Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA   Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA   Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA   Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA   Whitehead S., Barrell B.G.;
RT   "Complete genome sequence of a multiple drug resistant Salmonella
RT   enterica serovar Typhi CT18.";
RL   Nature 413:848-852(2001).
DR   EMBL; AL627274; CAD07625.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   313 AA;  34921 MW;  EA15DC17146DDDB5 CRC64;

  Query Match             33.9%;  Score 38;  DB 16;  Length 313;
  Best Local Similarity   34.8%;  Pred. No. 36;
  Matches    8;  Conservative    4;  Mismatches   11;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLXGGXSSGA 34
              |: | :|: |    :  | | ||
Db         53 KEMERDAMALLWSAIAAGLSMGA 75


Search completed: June 24, 2003, 23:07:40
Job time : 51.5 secs
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RP   SEQUENCE FROM N.A.
RC   STRAIN=C57;
RX   MEDLINE=20179892; PubMed=10713105;
RA   Fedele M., Benvenuto G., Pero R., Majello B., Battista S., Lembo F.,
RA   Vollono E., Day P.M., Santoro M., Lania L., Bruni C.B., Fusco A.,
RA   Chiatiotti L.;
RT   "A novel member of the BTB/POZ family, PATZ, associates with the RNF4
RT   RING finger protein and acts as a transcriptional repressor.";
RL   J. Biol. Chem. 275:7894-7901(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57;
RA   Chiariotti L., Fedele M.;
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF119255; AAF32517.1; -.
DR   MGD; MGI:1891832; Zfp278.
DR   InterPro; IPR000637; AT_hook.
DR   InterPro; IPR000822; Znf_C2H2.
DR   Pfam; PF02178; AT_hook; 1.
DR   Pfam; PF00096; zf-C2H2; 1.
DR   SMART; SM00384; AT_hook; 1.
DR   SMART; SM00355; ZnF_C2H2; 1.
DR   PROSITE; PS00354; HMGI_Y; 1.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
KW   DNA-binding; Metal-binding; Zinc-finger.
FT   NON_TER       1      1
FT   NON_TER     163    163
SQ   SEQUENCE   163 AA;  17227 MW;  60A3046938B4FC9D CRC64;

  Query Match             33.9%;  Score 38;  DB 11;  Length 163;
  Best Local Similarity   42.9%;  Pred. No. 17;
  Matches    9;  Conservative    1;  Mismatches   11;  Indels    0;  Gaps    0;

Qy         11 SKQXEEEAVRLXXXXLXGGXS 31
              | | |||| |     : | |
Db          2 SMQPEEEAARATGAAIAGQAS 22


RESULT 11
O58594
ID   O58594      PRELIMINARY;      PRT;   208 AA.
AC   O58594;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   208AA long hypothetical transcription initiation factor IIB.
GN   PH0864.
OS   Pyrococcus horikoshii.
OC   Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC   Pyrococcus.
OX   NCBI_TaxID=53953;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=OT3;
RX   MEDLINE=98344137; PubMed=9679194;
RA   Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA   Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA   Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA   Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA   Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA   Masuchi Y., Shizuya H., Kikuchi H.;
RT   "Complete sequence and gene organization of the genome of a hyper-
RT   thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
RL   DNA Res. 5:55-76(1998).
DR   EMBL; AP000003; BAA29958.1; -.
DR   HSSP; P29095; 1AIS.
DR   InterPro; IPR004366; Cyclin.
DR   InterPro; IPR000812; TFIIB_euk.
DR   Pfam; PF00382; transcript_fac2; 2.
DR   SMART; SM00385; CYCLIN; 2.
DR   PROSITE; PS00782; TFIIB; 1.
KW   Initiation factor; Complete proteome.
SQ   SEQUENCE   208 AA;  23878 MW;  CBE1A3D30CC76762 CRC64;

  Query Match             33.9%;  Score 38;  DB 17;  Length 208;
  Best Local Similarity   36.4%;  Pred. No. 23;
  Matches    8;  Conservative    3;  Mismatches   11;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLXGGXSSG 33
              |  | ||||:    :  | : |
Db         38 KHVEREAVRIYRKLIKSGVTKG 59


RESULT 12
O70379
ID   O70379      PRELIMINARY;      PRT;   289 AA.
AC   O70379;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Thioredoxin-related protein.
GN   TXNL.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98334653; PubMed=9668102;
RA   Lee K.K., Murakawa M., Takahashi S., Tsubuki S., Kawashima Si.,
RA   Sakamaki K., Yonehara S.;
RT   "Purification, molecular cloning, and characterization of TRP32, a
RT   novel thioredoxin-related mammalian protein of 32 kDa.";
RL   J. Biol. Chem. 273:19160-19166(1998).
DR   EMBL; AF052660; AAC40183.1; -.
DR   HSSP; O43396; 1GH2.
DR   MGD; MGI:1860078; Txnl.
DR   InterPro; IPR000063; Thiored.
DR   Pfam; PF00085; thiored; 1.
DR   PROSITE; PS00194; THIOREDOXIN; UNKNOWN_1.
SQ   SEQUENCE   289 AA;  32251 MW;  0AA39C6C1D1DFD0D CRC64;

  Query Match             33.9%;  Score 38;  DB 11;  Length 289;
  Best Local Similarity   44.4%;  Pred. No. 33;
  Matches    8;  Conservative    1;  Mismatches    9;  Indels    0;  Gaps    0;

Qy         11 SKQXEEEAVRLXXXXLXG 28
              ||| |||  |:      |
Db        250 SKQGEEETTRISYFTFIG 267


RESULT 13
Q8XCN1
ID   Q8XCN1      PRELIMINARY;      PRT;   310 AA.
AC   Q8XCN1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Putative transport.
GN   YFDC OR Z3611 OR ECS3230.
OS   Escherichia coli O157:H7.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=83334;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX   MEDLINE=21074935; PubMed=11206551;
RA   Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA   Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA   Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA   Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA   Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA   Welch R.A., Blattner F.R.;
RT   "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
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RX   MEDLINE=21016719; PubMed=11130712;
RA   Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA   White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA   Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA   Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA   Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA   Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA   Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA   Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA   Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA   Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA   Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA   Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA   Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA   Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA   Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA   Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT   "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 408:816-820(2000).
DR   EMBL; AC051630; AAG51222.1; -.
DR   InterPro; IPR002088; PPTA.
DR   InterPro; IPR001214; SET.
DR   InterPro; IPR001440; TPR.
DR   Pfam; PF00515; TPR; 4.
DR   SMART; SM00028; TPR; 4.
DR   PROSITE; PS00904; PPTA; UNKNOWN_1.
DR   PROSITE; PS50280; SET; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   781 AA;  87145 MW;  F27B02CA82C35C76 CRC64;

  Query Match             34.8%;  Score 39;  DB 10;  Length 781;
  Best Local Similarity   50.0%;  Pred. No. 63;
  Matches    9;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         17 EAVRLXXXXLXGGXSSGA 34
              | |:|    |  | ||||
Db        722 EMVKLASIQLASGDSSGA 739


RESULT 8
Q95DV5
ID   Q95DV5      PRELIMINARY;      PRT;   468 AA.
AC   Q95DV5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   FtsZ-like protein.
GN   FTSZ.
OS   Nicotiana tabacum (Common tobacco).
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX   NCBI_TaxID=4097;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. BRIGHT YELLOW 2;
RA   Falconet D.R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. BRIGHT YELLOW 2;
RA   El Shami M.;
RL   Thesis (2000), Department of Biological Sciences,
RL   University of Grenoble, Grenoble, France.
DR   EMBL; AJ311847; CAC44257.1; -.
DR   InterPro; IPR000158; FtsZ.
DR   InterPro; IPR003008; Tubulin_FtsZ.
DR   Pfam; PF00091; tubulin; 1.
DR   TIGRFAMs; TIGR00065; ftsZ; 1.
DR   PROSITE; PS01135; FTSZ_2; UNKNOWN_1.
KW   Chloroplast; GTP-binding.
SQ   SEQUENCE   468 AA;  49174 MW;  8237DF472D92257F CRC64;

  Query Match             34.4%;  Score 38.5;  DB 8;  Length 468;
  Best Local Similarity   33.3%;  Pred. No. 45;
  Matches   12;  Conservative    2;  Mismatches   17;  Indels    5;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVR-----LXXXXLXGGXSSGA 34
              |      |||  ||||          : ||  :||
Db        176 GMNAANESKQAIEEAVYGADMVFVTAGMGGGTGTGA 211


RESULT 9
Q9M436
ID   Q9M436      PRELIMINARY;      PRT;   468 AA.
AC   Q9M436;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chloroplast cell division protein ftsZ.
GN   FTSZ.
OS   Nicotiana tabacum (Common tobacco).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX   NCBI_TaxID=4097;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   El-Shami M., Alcaraz J.P., Lerbs-Mache S., Falconet D.;
RT   "A new cDNA encoding FtsZ-like protein from Nicotiana tabacum.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: THIS PROTEIN IS ESSENTIAL TO THE CELL-DIVISION PROCESS.
CC       ITS SEEMS TO ASSEMBLE INTO A DYNAMIC RING ON THE INNER SURFACE OF
CC       THE CYTOPLASMIC MEMBRANE AT THE PLACE WHERE DIVISION WILL OCCUR,
CC       AND THE FORMATION OF THE RING IS THE SIGNAL FOR SEPTATION TO
CC       BEGIN. BINDS TO AND HYDROLYZES GTP (BY SIMILARITY).
CC   -!- SUBUNIT: AGGREGATE TO FORM A RING-LIKE STRUCTURE (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC. ASSEMBLE AT THE INNER SURFACE
CC       OF THE CYTOPLASMIC MEMBRANE (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE FTSZ FAMILY.
DR   EMBL; AJ271750; CAB89288.1; -.
DR   HSSP; Q57816; 1FSZ.
DR   InterPro; IPR000158; FtsZ.
DR   InterPro; IPR003008; Tubulin_FtsZ.
DR   Pfam; PF00091; tubulin; 1.
DR   PRINTS; PR00423; CELLDVISFTSZ.
DR   TIGRFAMs; TIGR00065; ftsZ; 1.
DR   PROSITE; PS01135; FTSZ_2; 1.
KW   Cell division; GTP-binding; Septation.
SQ   SEQUENCE   468 AA;  49274 MW;  C216D6B2DE167ED3 CRC64;

  Query Match             34.4%;  Score 38.5;  DB 10;  Length 468;
  Best Local Similarity   33.3%;  Pred. No. 45;
  Matches   12;  Conservative    2;  Mismatches   17;  Indels    5;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVR-----LXXXXLXGGXSSGA 34
              |      |||  ||||          : ||  :||
Db        176 GMNAANESKQAIEEAVYGADMVFVTAGMGGGTGTGA 211


RESULT 10
Q9JLY9
ID   Q9JLY9      PRELIMINARY;      PRT;   163 AA.
AC   Q9JLY9;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   PATZ (Fragment).
GN   ZFP278 OR PATZ.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
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RA   Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA   Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA   Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA   Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA   Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA   Cielo C., Slater S.;
RT   "Genome sequence of the plant pathogen and biotechnology agent
RT   Agrobacterium tumefaciens C58.";
RL   Science 294:2323-2328(2001).
DR   EMBL; AE009224; AAL43746.1; -.
DR   EMBL; AE008190; AAK88480.1; -.
KW   Complete proteome.
SQ   SEQUENCE   189 AA;  21150 MW;  785D4F2AA10A3DC4 CRC64;

  Query Match             34.8%;  Score 39;  DB 16;  Length 189;
  Best Local Similarity   43.5%;  Pred. No. 13;
  Matches   10;  Conservative    1;  Mismatches   12;  Indels    0;  Gaps    0;

Qy         11 SKQXEEEAVRLXXXXLXGGXSSG 33
              :|  | |||||    |  |   |
Db        154 NKMSETEAVRLVEVNLAKGPKRG 176


RESULT 5
Q98FB1
ID   Q98FB1      PRELIMINARY;      PRT;   193 AA.
AC   Q98FB1;
DT   01-OCT-2001 (TrEMBLrel. 18, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   Transcriptional factor regulator.
GN   MLR3857.
OS   Rhizobium loti (Mesorhizobium loti).
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Phyllobacteriaceae; Mesorhizobium.
OX   NCBI_TaxID=381;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MAFF303099;
RX   MEDLINE=21082930; PubMed=11214968;
RA   Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA   Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA   Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA   Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA   Takeuchi C., Yamada M., Tabata S.;
RT   "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT   Mesorhizobium loti.";
RL   DNA Res. 7:331-338(2000).
DR   EMBL; AP003002; BAB50656.1; -.
DR   InterPro; IPR003711; CarD.
DR   Pfam; PF02559; TF_CarD; 1.
KW   Complete proteome.
SQ   SEQUENCE   193 AA;  21811 MW;  53B7FFCCE907B538 CRC64;

  Query Match             34.8%;  Score 39;  DB 16;  Length 193;
  Best Local Similarity   41.7%;  Pred. No. 13;
  Matches   10;  Conservative    2;  Mismatches   12;  Indels    0;  Gaps    0;

Qy         11 SKQXEEEAVRLXXXXLXGGXSSGA 34
              ::  | |||||    |  |   ||
Db        157 NRMSETEAVRLIEVNLNKGPKRGA 180


RESULT 6
Q9RD53
ID   Q9RD53      PRELIMINARY;      PRT;   369 AA.
AC   Q9RD53;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Putative transcriptional regulator.
GN   SCO0629 OR SCF56.13C.
OS   Streptomyces coelicolor.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1902;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RA   Murphy L., Harris D.;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RA   Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RX   MEDLINE=97000351; PubMed=8843436;
RA   Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
RA   Kinashi H., Hopwood D.A.;
RT   "A set of ordered cosmids and a detailed genetic and physical map for
RT   the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL   Mol. Microbiol. 21:77-96(1996).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2) / M145;
RA   Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA   Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA   Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA   Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA   Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA   Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA   Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA   Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA   Hopwood D.A.;
RT   "Complete genome sequence of the model actinomycete Streptomyces
RT   coelicolor A3(2).";
RL   Nature 417:141-147(2002).
DR   EMBL; AL133424; CAB62758.1; -.
DR   HSSP; P03023; 1LQC.
DR   InterPro; IPR000843; HTH_LacI.
DR   InterPro; IPR001993; Mitoch_carrier.
DR   InterPro; IPR001761; PeriplaBP/LacI.
DR   Pfam; PF00532; Peripla_BP_like; 1.
DR   SMART; SM00354; HTH_LACI; 1.
DR   PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
SQ   SEQUENCE   369 AA;  37741 MW;  519C78F8D9A04EE9 CRC64;

  Query Match             34.8%;  Score 39;  DB 16;  Length 369;
  Best Local Similarity   47.1%;  Pred. No. 27;
  Matches    8;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         17 EAVRLXXXXLXGGXSSG 33
              |||||    : || : |
Db        334 EAVRLLATRIAGGPAEG 350


RESULT 7
Q9C812
ID   Q9C812      PRELIMINARY;      PRT;   781 AA.
AC   Q9C812;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Hypothetical 87.1 kDa protein.
GN   F10C21.7.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
```

```
CC       BEGIN. BINDS TO AND HYDROLYZES GTP (BY SIMILARITY).
CC    -!- SUBUNIT: AGGREGATE TO FORM A RING-LIKE STRUCTURE (BY SIMILARITY).
CC    -!- SUBCELLULAR LOCATION: CYTOPLASMIC. ASSEMBLE AT THE INNER SURFACE
CC       OF THE CYTOPLASMIC MEMBRANE (BY SIMILARITY).
CC    -!- SIMILARITY: BELONGS TO THE FTSZ FAMILY.
DR   EMBL; AJ001586; CAA04845.2; -.
DR   EMBL; AJ249138; CAB54558.1; -.
DR   HSSP; Q57816; 1FSZ.
DR   InterPro; IPR000158; FtsZ.
DR   InterPro; IPR003008; Tubulin_FtsZ.
DR   Pfam; PF00091; tubulin; 1.
DR   PRINTS; PR00423; CELLDVISFTSZ.
DR   TIGRFAMs; TIGR00065; ftsZ; 1.
DR   PROSITE; PS01135; FTSZ_2; 1.
KW   Cell division; GTP-binding; Septation; Transit peptide.
FT   TRANSIT       1     31       POTENTIAL.
FT   CHAIN        32    458       PLASTID DIVISION PROTEIN FTSZ1.
SQ   SEQUENCE   458 AA;  47536 MW;  85FB9B78CB098B4F CRC64;

  Query Match             36.2%;  Score 40.5;  DB 10;  Length 458;
  Best Local Similarity   33.3%;  Pred. No. 18;
  Matches   12;  Conservative    2;  Mismatches   17;  Indels    5;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVR-----LXXXXLXGGXSSGA 34
              |      ||   |||:|         : ||  |||
Db        169 GCSAAEESKAMVEEALRGADMVFVTAGMGGGTGSGA 204


RESULT 2
Q9LDK5
ID   Q9LDK5      PRELIMINARY;      PRT;   464 AA.
AC   Q9LDK5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Plastid division protein ftsZ2 precursor.
GN   FTSZ.
OS   Physcomitrella patens (Moss).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC   Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
OX   NCBI_TaxID=3218;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kruse S., Kiessling J., Harter K., Rensing S., Decker E., Reski R.;
RT   "Two distinct nuclear-encoded plant ftsZ-genes are highly conserved,
RT   both their encoded proteins are importedinto chloroplasts and both are
RT   indispensable for plastid division.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ249140; CAB76387.1; -.
DR   EMBL; AJ249139; CAB76386.1; -.
DR   HSSP; Q57816; 1FSZ.
DR   InterPro; IPR000158; FtsZ.
DR   InterPro; IPR000217; Tubulin.
DR   InterPro; IPR003008; Tubulin_FtsZ.
DR   Pfam; PF00091; tubulin; 1.
DR   PRINTS; PR00423; CELLDVISFTSZ.
DR   TIGRFAMs; TIGR00065; ftsZ; 1.
DR   PROSITE; PS01135; FTSZ_2; 1.
DR   PROSITE; PS00227; TUBULIN; UNKNOWN_1.
KW   GTP-binding; Transit peptide.
FT   TRANSIT       1     39       POTENTIAL.
FT   CHAIN        40    464       PLASTID DIVISION PROTEIN FTSZ2.
SQ   SEQUENCE   464 AA;  48423 MW;  8D6659C5D2D6C0D3 CRC64;

  Query Match             36.2%;  Score 40.5;  DB 10;  Length 464;
  Best Local Similarity   33.3%;  Pred. No. 18;
  Matches   12;  Conservative    2;  Mismatches   17;  Indels    5;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVR-----LXXXXLXGGXSSGA 34
              |      ||   |||:|         : ||  |||
Db        177 GCSAAEESKAMVEEALRGADMVFVTAGMGGGTGSGA 212


RESULT 3
Q97AK4
ID   Q97AK4      PRELIMINARY;      PRT;   347 AA.
AC   Q97AK4;
DT   01-OCT-2001 (TrEMBLrel. 18, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Cell division protein.
GN   TV0806 OR TVG0806423.
OS   Thermoplasma volcanium.
OC   Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC   Thermoplasmataceae; Thermoplasma.
OX   NCBI_TaxID=50339;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GSS1 / DSM 4299 / JCM 9571;
RX   MEDLINE=20570466; PubMed=11121031;
RA   Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
RA   Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
RA   Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
RT   "Archaeal adaptation to higher temperatures revealed by genomic
RT   sequence of Thermoplasma volcanium.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
DR   EMBL; AP000993; BAB59948.1; -.
DR   InterPro; IPR000158; FtsZ.
DR   InterPro; IPR003008; Tubulin_FtsZ.
DR   Pfam; PF00091; tubulin; 1.
DR   PRINTS; PR00423; CELLDVISFTSZ.
DR   TIGRFAMs; TIGR00065; ftsZ; 1.
KW   Complete proteome.
SQ   SEQUENCE   347 AA;  37421 MW;  5CC382D1BFA82331 CRC64;

  Query Match             35.7%;  Score 40;  DB 17;  Length 347;
  Best Local Similarity   34.8%;  Pred. No. 16;
  Matches    8;  Conservative    4;  Mismatches   11;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLXGGXSSGA 34
              || :| ::      | ||  :||
Db        108 KQIDETSIVFITAGLGGGTGTGA 130


RESULT 4
Q8UBT5
ID   Q8UBT5      PRELIMINARY;      PRT;   189 AA.
AC   Q8UBT5;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Transcriptional regulator, CarD family.
GN   ATU2765 OR AGR_C_5013.
OS   Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Rhizobiaceae; Rhizobium.
OX   NCBI_TaxID=176299;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21608550; PubMed=11743193;
RA   Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA   Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA   Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA   Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA   Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA   Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA   Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA   Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA   Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA   Nester E.W.;
RT   "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT   C58.";
RL   Science 294:2317-2323(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21608551; PubMed=11743194;
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OM protein - protein search, using sw model

Run on: June 24, 2003, 23:02:15 ; Search time 49.5 Seconds
(without alignments)
166.503 Million cell updates/sec

Title: US-09-889-331A-48
Perfect score: 112
Sequence: 1 XXXGTXXXXXSKQXEEEAVRLXXXXLXGGXSSGAXXXXXX 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	40.5	36.2	458	10	O49922	O49922 physcomitre
2	40.5	36.2	464	10	Q9LDK5	Q9ldk5 physcomitre
3	40	35.7	347	17	Q97AK4	Q97ak4 thermoplasm
4	39	34.8	189	16	Q8UBT5	Q8ubt5 agrobacteri
5	39	34.8	193	16	Q98FB1	Q98fb1 rhizobium l
6	39	34.8	369	16	Q9RD53	Q9rd53 streptomyce
7	39	34.8	781	10	Q9C812	Q9c812 arabidopsis
8	38.5	34.4	468	8	Q95DV5	Q95dv5 nicotiana t
9	38.5	34.4	468	10	Q9M436	Q9m436 nicotiana t
10	38	33.9	163	11	Q9JLY9	Q9jly9 mus musculu
11	38	33.9	208	17	O58594	O58594 pyrococcus
12	38	33.9	289	11	O70379	O70379 mus musculu
13	38	33.9	310	16	Q8XCN1	Q8xcn1 escherichia
14	38	33.9	313	16	Q8ZNA4	Q8zna4 salmonella
15	38	33.9	313	16	Q8Z4Y7	Q8z4y7 salmonella
16	38	33.9	317	10	Q94D21	Q94d21 oryza sativ
17	38	33.9	424	4	Q9HD72	Q9hd72 homo sapien
18	38	33.9	537	4	Q9P1A9	Q9p1a9 homo sapien
19	38	33.9	537	4	Q9HBE2	Q9hbe2 homo sapien
20	38	33.9	537	4	Q9HBE3	Q9hbe3 homo sapien
21	38	33.9	616	4	Q9Y529	Q9y529 homo sapien
22	38	33.9	631	2	Q8RM05	Q8rm05 xanthobacte
23	38	33.9	641	4	Q9UDU0	Q9udu0 homo sapien
24	38	33.9	641	11	Q9JMG9	Q9jmg9 mus musculu
25	38	33.9	687	4	Q9HBE1	Q9hbe1 homo sapien
26	37.5	33.5	478	16	Q8XZE5	Q8xze5 ralstonia s
27	37.5	33.5	785	12	P89451	P89451 herpes simp
28	37	33.0	207	16	Q8YJ08	Q8yj08 brucella me
29	37	33.0	246	4	Q9H6G1	Q9h6g1 homo sapien
30	37	33.0	251	4	Q9BU05	Q9bu05 homo sapien
31	37	33.0	251	4	Q9BWR9	Q9bwr9 homo sapien
32	37	33.0	264	4	Q96H23	Q96h23 homo sapien
33	37	33.0	328	10	O50007	O50007 hordeum vul
34	37	33.0	356	17	Q980M3	Q980m3 sulfolobus
35	37	33.0	393	4	Q96SD6	Q96sd6 homo sapien
36	37	33.0	470	4	Q9NVQ6	Q9nvq6 homo sapien
37	37	33.0	470	4	Q96TC7	Q96tc7 homo sapien
38	37	33.0	492	16	Q9F3D1	Q9f3d1 streptomyce
39	37	33.0	524	11	Q9R027	Q9r027 mus musculu
40	37	33.0	850	5	Q24211	Q24211 drosophila
41	37	33.0	850	5	Q9W5M8	Q9w5m8 drosophila
42	37	33.0	880	12	Q9DWB5	Q9dwb5 rat cytomeg
43	37	33.0	1041	16	Q981Z6	Q981z6 rhizobium l
44	36.5	32.6	124	16	Q9X8X6	Q9x8x6 streptomyce
45	36.5	32.6	456	3	Q06821	Q06821 saccharomyc

ALIGNMENTS

```
RESULT 1
O49922
ID   O49922      PRELIMINARY;      PRT;   458 AA.
AC   O49922;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Cell division protein ftsZ precursor.
GN   FTSZ.
OS   Physcomitrella patens (Moss).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC   Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
OX   NCBI_TaxID=3218;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Reski R.;
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98208546; PubMed=9539743;
RA   Strepp R., Scholz S., Kruse S., Speth V., Reski R.;
RT   "Plant nuclear gene knockout reveals a role in plastid division of the
RT   bacterial cell division protein FtsZ, an ancestral tubulin.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:4368-4373(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Reski R.;
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Kruse S., Kiessling J., Harter K., Rensing S., Decker E., Reski R.;
RT   "Two distinct nuclear-encoded plant ftsz-genes are highly conserved,
RT   both their encoded proteins are importedinto chloroplasts and both are
RT   indispensable for plastid division.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: THIS PROTEIN IS ESSENTIAL TO THE CELL-DIVISION PROCESS.
CC       ITS SEEMS TO ASSEMBLE INTO A DYNAMIC RING ON THE INNER SURFACE OF
CC       THE CYTOPLASMIC MEMBRANE AT THE PLACE WHERE DIVISION WILL OCCUR,
CC       AND THE FORMATION OF THE RING IS THE SIGNAL FOR SEPTATION TO
```

```
;   NAME/KEY: MOD_RES
;   LOCATION: 40
;   OTHER INFORMATION: Xaa represents Lys(E-MPA)-NH2-5TFA and where "E" represents Epsil
US-09-623-618B-31

  Query Match            75.2%;  Score 91;  DB 4;  Length 40;
  Best Local Similarity  65.6%;  Pred. No. 8.9e-10;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| ||||||| |||||  ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 14
US-09-623-618B-32
; Sequence 32, Application US/09623618B
; Patent No. 6329336
; GENERAL INFORMATION:
;  APPLICANT: Bridon, Dominique P.
;  APPLICANT:  L'Archeveque, Benoit
;  APPLICANT:  Ezrin, Alan M.
;  APPLICANT:  Holmes, Darren L.
;  APPLICANT:  Leblanc, Anouk
;  APPLICANT:  St. Pierre, Serge
;  TITLE OF INVENTION: LONG LASTING INSULINOTROPIC PEPTIDES
;  FILE REFERENCE: 500862001620
;  CURRENT APPLICATION NUMBER: US/09/623,618B
;  CURRENT FILING DATE:  2000-09-05
;  PRIOR APPLICATION NUMBER: PCT/US00/13563
;  PRIOR FILING DATE: 2000-05-17
;  PRIOR APPLICATION NUMBER: 60/159,783
;  PRIOR FILING DATE: 1999-10-15
;  PRIOR APPLICATION NUMBER: 60/134,406
;  PRIOR FILING DATE: 1999-05-17
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
;   NAME/KEY: MOD_RES
;   LOCATION: 40
;   OTHER INFORMATION: Xaa represents Lys(E-AEEA-AEEA-MPA)-NH2-5TFA and where "E" repres
US-09-623-618B-32

  Query Match            75.2%;  Score 91;  DB 4;  Length 40;
  Best Local Similarity  65.6%;  Pred. No. 8.9e-10;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| ||||||| |||||  ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 15
US-09-623-618B-33
; Sequence 33, Application US/09623618B
; Patent No. 6329336
; GENERAL INFORMATION:
;  APPLICANT: Bridon, Dominique P.
;  APPLICANT:  L'Archeveque, Benoit
;  APPLICANT:  Ezrin, Alan M.
;  APPLICANT:  Holmes, Darren L.
;  APPLICANT:  Leblanc, Anouk
;  APPLICANT:  St. Pierre, Serge
;  TITLE OF INVENTION: LONG LASTING INSULINOTROPIC PEPTIDES
;  FILE REFERENCE: 500862001620
;  CURRENT APPLICATION NUMBER: US/09/623,618B
;  CURRENT FILING DATE:  2000-09-05
;  PRIOR APPLICATION NUMBER: PCT/US00/13563
;  PRIOR FILING DATE: 2000-05-17
;  PRIOR APPLICATION NUMBER: 60/159,783
;  PRIOR FILING DATE: 1999-10-15
;  PRIOR APPLICATION NUMBER: 60/134,406
;  PRIOR FILING DATE: 1999-05-17
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
;   NAME/KEY: MOD_RES
;   LOCATION: 40
;   OTHER INFORMATION: Xaa represents Lys(E-MPA)-NH2-5TFA and where "E" represents Ep
US-09-623-618B-33

  Query Match            75.2%;  Score 91;  DB 4;  Length 40;
  Best Local Similarity  65.6%;  Pred. No. 8.9e-10;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| ||||||| |||||  ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


Search completed: June 24, 2003, 23:09:16
Job time : 18.5 secs
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RESULT 10
US-09-303-016-9
; Sequence 9, Application US/09303016
; Patent No. 6429197
; GENERAL INFORMATION:
;  APPLICANT:  Coolidge, Thomas R.
;  APPLICANT:  Ehlers, Mario R.W.
;  TITLE OF INVENTION:  Metabolic Intervention with GLP-1 or its Biologically
;  TITLE OF INVENTION:  Active Analogues to Improve the Function of the
;  TITLE OF INVENTION:  Ischemic and Reperfused Brain
;  FILE REFERENCE:  P03660US2
;  CURRENT APPLICATION NUMBER: US/09/303,016
;  CURRENT FILING DATE:  1999-04-30
;  PRIOR APPLICATION NUMBER:  60/103,498
;  PRIOR FILING DATE:  1998-10-08
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 39
;   TYPE: PRT
;   ORGANISM: Heloderma suspectum
US-09-303-016-9

  Query Match           75.2%;  Score 91;  DB 4;  Length 39;
  Best Local Similarity   65.6%;  Pred. No. 8.7e-10;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| ||||||||    ||||| ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 11
US-09-623-618B-18
; Sequence 18, Application US/09623618B
; Patent No. 6329336
; GENERAL INFORMATION:
;  APPLICANT: Bridon, Dominique P.
;  APPLICANT:  L'Archeveque, Benoit
;  APPLICANT:  Ezrin, Alan M.
;  APPLICANT:  Holmes, Darren L.
;  APPLICANT:  Leblanc, Anouk
;  APPLICANT:  St. Pierre, Serge
;  TITLE OF INVENTION: LONG LASTING INSULINOTROPIC PEPTIDES
;  FILE REFERENCE: 500862001620
;  CURRENT APPLICATION NUMBER: US/09/623,618B
;  CURRENT FILING DATE:  2000-09-05
;  PRIOR APPLICATION NUMBER: PCT/US00/13563
;  PRIOR FILING DATE: 2000-05-17
;  PRIOR APPLICATION NUMBER: 60/159,783
;  PRIOR FILING DATE: 1999-10-15
;  PRIOR APPLICATION NUMBER: 60/134,406
;  PRIOR FILING DATE: 1999-05-17
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-09-623-618B-18

  Query Match           75.2%;  Score 91;  DB 4;  Length 40;
  Best Local Similarity   65.6%;  Pred. No. 8.9e-10;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| ||||||||    ||||| ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 12
US-09-623-618B-19
; Sequence 19, Application US/09623618B
; Patent No. 6329336
; GENERAL INFORMATION:
;  APPLICANT: Bridon, Dominique P.
;  APPLICANT:  L'Archeveque, Benoit
;  APPLICANT:  Ezrin, Alan M.
;  APPLICANT:  Holmes, Darren L.
;  APPLICANT:  Leblanc, Anouk
;  APPLICANT:  St. Pierre, Serge
;  TITLE OF INVENTION: LONG LASTING INSULINOTROPIC PEPTIDES
;  FILE REFERENCE: 500862001620
;  CURRENT APPLICATION NUMBER: US/09/623,618B
;  CURRENT FILING DATE:  2000-09-05
;  PRIOR APPLICATION NUMBER: PCT/US00/13563
;  PRIOR FILING DATE: 2000-05-17
;  PRIOR APPLICATION NUMBER: 60/159,783
;  PRIOR FILING DATE: 1999-10-15
;  PRIOR APPLICATION NUMBER: 60/134,406
;  PRIOR FILING DATE: 1999-05-17
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-09-623-618B-19

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  Best Local Similarity   65.6%;  Pred. No. 8.9e-10;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
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Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 13
US-09-623-618B-31
; Sequence 31, Application US/09623618B
; Patent No. 6329336
; GENERAL INFORMATION:
;  APPLICANT: Bridon, Dominique P.
;  APPLICANT:  L'Archeveque, Benoit
;  APPLICANT:  Ezrin, Alan M.
;  APPLICANT:  Holmes, Darren L.
;  APPLICANT:  Leblanc, Anouk
;  APPLICANT:  St. Pierre, Serge
;  TITLE OF INVENTION: LONG LASTING INSULINOTROPIC PEPTIDES
;  FILE REFERENCE: 500862001620
;  CURRENT APPLICATION NUMBER: US/09/623,618B
;  CURRENT FILING DATE:  2000-09-05
;  PRIOR APPLICATION NUMBER: PCT/US00/13563
;  PRIOR FILING DATE: 2000-05-17
;  PRIOR APPLICATION NUMBER: 60/159,783
;  PRIOR FILING DATE: 1999-10-15
;  PRIOR APPLICATION NUMBER: 60/134,406
;  PRIOR FILING DATE: 1999-05-17
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-09-623-618B-11

  Query Match             75.2%;  Score 91;  DB 4;  Length 39;
  Best Local Similarity   65.6%;  Pred. No. 8.7e-10;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
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Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 6
US-09-623-618B-12
; Sequence 12, Application US/09623618B
; Patent No. 6329336
; GENERAL INFORMATION:
;  APPLICANT: Bridon, Dominique P.
;  APPLICANT:  L'Archeveque, Benoit
;  APPLICANT:  Ezrin, Alan M.
;  APPLICANT:  Holmes, Darren L.
;  APPLICANT:  Leblanc, Anouk
;  APPLICANT:  St. Pierre, Serge
;  TITLE OF INVENTION: LONG LASTING INSULINOTROPIC PEPTIDES
;  FILE REFERENCE: 500862001620
;  CURRENT APPLICATION NUMBER: US/09/623,618B
;  CURRENT FILING DATE:  2000-09-05
;  PRIOR APPLICATION NUMBER: PCT/US00/13563
;  PRIOR FILING DATE: 2000-05-17
;  PRIOR APPLICATION NUMBER: 60/159,783
;  PRIOR FILING DATE: 1999-10-15
;  PRIOR APPLICATION NUMBER: 60/134,406
;  PRIOR FILING DATE: 1999-05-17
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 39
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-09-623-618B-12

  Query Match             75.2%;  Score 91;  DB 4;  Length 39;
  Best Local Similarity   65.6%;  Pred. No. 8.7e-10;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||| ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 7
US-09-333-415-7
; Sequence 7, Application US/09333415
; Patent No. 6344180
; GENERAL INFORMATION:
;  APPLICANT:  Holst, Jens J.
;  APPLICANT:  Vilsboll, Tina
;  TITLE OF INVENTION:  GLP-1 as a Diagnostic Test to Determine Beta-Cell
;  TITLE OF INVENTION:  Function and the Presence of the Condition of IGT and
;  TITLE OF INVENTION:  Type-II Diabetes
;  FILE REFERENCE:  P03987US0
;  CURRENT APPLICATION NUMBER: US/09/333,415
;  CURRENT FILING DATE:  1999-06-15
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 39
;   TYPE: PRT
;   ORGANISM: Heloderma suspectum
US-09-333-415-7

  Query Match             75.2%;  Score 91;  DB 4;  Length 39;
  Best Local Similarity   65.6%;  Pred. No. 8.7e-10;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||| ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 8
US-09-333-415-9
; Sequence 9, Application US/09333415
; Patent No. 6344180
; GENERAL INFORMATION:
;  APPLICANT:  Holst, Jens J.
;  APPLICANT:  Vilsboll, Tina
;  TITLE OF INVENTION:  GLP-1 as a Diagnostic Test to Determine Beta-Cell
;  TITLE OF INVENTION:  Function and the Presence of the Condition of IGT and
;  TITLE OF INVENTION:  Type-II Diabetes
;  FILE REFERENCE:  P03987US0
;  CURRENT APPLICATION NUMBER: US/09/333,415
;  CURRENT FILING DATE:  1999-06-15
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 39
;   TYPE: PRT
;   ORGANISM: Heloderma suspectum
US-09-333-415-9

  Query Match             75.2%;  Score 91;  DB 4;  Length 39;
  Best Local Similarity   65.6%;  Pred. No. 8.7e-10;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||| ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 9
US-09-303-016-7
; Sequence 7, Application US/09303016
; Patent No. 6429197
; GENERAL INFORMATION:
;  APPLICANT:  Coolidge, Thomas R.
;  APPLICANT:  Ehlers, Mario R.W.
;  TITLE OF INVENTION:  Metabolic Intervention with GLP-1 or its Biologically
;  TITLE OF INVENTION:  Active Analogues to Improve the Function of the
;  TITLE OF INVENTION:  Ischemic and Reperfused Brain
;  FILE REFERENCE:  P03660US2
;  CURRENT APPLICATION NUMBER: US/09/303,016
;  CURRENT FILING DATE:  1999-04-30
;  PRIOR APPLICATION NUMBER:  60/103,498
;  PRIOR FILING DATE:  1998-10-08
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 39
;   TYPE: PRT
;   ORGANISM: Heloderma suspectum
US-09-303-016-7

  Query Match             75.2%;  Score 91;  DB 4;  Length 39;
  Best Local Similarity   65.6%;  Pred. No. 8.7e-10;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
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Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35
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Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 2
US-08-066-480-2
; Sequence 2, Application US/08066480
; Patent No. 5424286
;  GENERAL INFORMATION:
;    APPLICANT:  Eng, John
;    TITLE OF INVENTION:  Pharmaceutical Compositions And Use of
;    TITLE OF INVENTION:  Exendin-3 and Exendin-4 for Treatment of Diabetes Mellitus
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Allegretti & Witcoff, Ltd.
;      STREET:  10 S. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/066,480
;      FILING DATE:  24-MAR-1993
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McDonnell, John J
;      REGISTRATION NUMBER:  26,949
;      REFERENCE/DOCKET NUMBER:  93,084
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-715-1000
;      TELEFAX:  312-715-1234
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..39
;      OTHER INFORMATION:  /label= Exendin-4
US-08-066-480-2

  Query Match             75.2%;  Score 91;  DB 1;  Length 39;
  Best Local Similarity   65.6%;  Pred. No. 8.7e-10;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||| ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 3
US-09-302-596-7
; Sequence 7, Application US/09302596
; Patent No. 6284725
; GENERAL INFORMATION:
;  APPLICANT: Coolidge, Thomas R.
;  APPLICANT:  Ehlers, Mario R.W.
;  TITLE OF INVENTION: Metabolic Intervention with GLP-1 to Improve the Function of
;  TITLE OF INVENTION:  Ischemic and Reperfused Tissue
;  FILE REFERENCE: P03660US1
;  CURRENT APPLICATION NUMBER: US/09/302,596
;  CURRENT FILING DATE:  1999-04-30
;  PRIOR APPLICATION NUMBER: 60/103,498
;  PRIOR FILING DATE: 1998-10-08
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 39
;   TYPE: PRT
;   ORGANISM: Gila Monster venom
US-09-302-596-7

  Query Match             75.2%;  Score 91;  DB 4;  Length 39;
  Best Local Similarity   65.6%;  Pred. No. 8.7e-10;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||| ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 4
US-09-302-596-9
; Sequence 9, Application US/09302596
; Patent No. 6284725
; GENERAL INFORMATION:
;  APPLICANT: Coolidge, Thomas R.
;  APPLICANT:  Ehlers, Mario R.W.
;  TITLE OF INVENTION: Metabolic Intervention with GLP-1 to Improve the Function of
;  TITLE OF INVENTION:  Ischemic and Reperfused Tissue
;  FILE REFERENCE: P03660US1
;  CURRENT APPLICATION NUMBER: US/09/302,596
;  CURRENT FILING DATE:  1999-04-30
;  PRIOR APPLICATION NUMBER: 60/103,498
;  PRIOR FILING DATE: 1998-10-08
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 39
;   TYPE: PRT
;   ORGANISM: Gila Monster venom
US-09-302-596-9

  Query Match             75.2%;  Score 91;  DB 4;  Length 39;
  Best Local Similarity   65.6%;  Pred. No. 8.7e-10;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
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Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 5
US-09-623-618B-11
; Sequence 11, Application US/09623618B
; Patent No. 6329336
; GENERAL INFORMATION:
;  APPLICANT: Bridon, Dominique P.
;  APPLICANT:  L'Archeveque, Benoit
;  APPLICANT:  Ezrin, Alan M.
;  APPLICANT:  Holmes, Darren L.
;  APPLICANT:  Leblanc, Anouk
;  APPLICANT:  St. Pierre, Serge
;  TITLE OF INVENTION: LONG LASTING INSULINOTROPIC PEPTIDES
;  FILE REFERENCE: 500862001620
;  CURRENT APPLICATION NUMBER: US/09/623,618B
;  CURRENT FILING DATE:  2000-09-05
;  PRIOR APPLICATION NUMBER: PCT/US00/13563
;  PRIOR FILING DATE: 2000-05-17
;  PRIOR APPLICATION NUMBER: 60/159,783
;  PRIOR FILING DATE: 1999-10-15
;  PRIOR APPLICATION NUMBER: 60/134,406
;  PRIOR FILING DATE: 1999-05-17
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 39
;   TYPE: PRT
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OM protein - protein search, using sw model

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(without alignments)
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Title: US-09-889-331A-47
Perfect score: 121
Sequence: 1 XXXGTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGAXXXXX 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	91	75.2	39	1	US-08-066-480-2	Sequence 2, Appli
3	91	75.2	39	4	US-09-302-596-7	Sequence 7, Appli
4	91	75.2	39	4	US-09-302-596-9	Sequence 9, Appli
5	91	75.2	39	4	US-09-623-618B-11	Sequence 11, Appl
6	91	75.2	39	4	US-09-623-618B-12	Sequence 12, Appl
7	91	75.2	39	4	US-09-333-415-7	Sequence 7, Appli
8	91	75.2	39	4	US-09-333-415-9	Sequence 9, Appli
9	91	75.2	39	4	US-09-303-016-7	Sequence 7, Appli
10	91	75.2	39	4	US-09-303-016-9	Sequence 9, Appli
11	91	75.2	40	4	US-09-623-618B-18	Sequence 18, Appl
12	91	75.2	40	4	US-09-623-618B-19	Sequence 19, Appl
13	91	75.2	40	4	US-09-623-618B-31	Sequence 31, Appl
14	91	75.2	40	4	US-09-623-618B-32	Sequence 32, Appl
15	91	75.2	40	4	US-09-623-618B-33	Sequence 33, Appl
16	91	75.2	40	4	US-09-623-618B-34	Sequence 34, Appl
17	83	68.6	31	1	US-08-066-480-5	Sequence 5, Appli
18	83	68.6	31	4	US-09-302-596-8	Sequence 8, Appli
19	83	68.6	31	4	US-09-623-618B-15	Sequence 15, Appl
20	83	68.6	31	4	US-09-623-618B-24	Sequence 24, Appl
21	83	68.6	31	4	US-09-333-415-8	Sequence 8, Appli
22	83	68.6	31	4	US-09-303-016-8	Sequence 8, Appli
23	75	62.0	31	1	US-08-066-480-3	Sequence 3, Appli
24	75	62.0	31	1	US-08-066-480-4	Sequence 4, Appli
25	75	62.0	31	4	US-09-623-618B-14	Sequence 14, Appl
26	75	62.0	31	4	US-09-623-618B-23	Sequence 23, Appl
27	75	62.0	32	4	US-09-623-618B-35	Sequence 35, Appl
28	62.5	51.7	29	4	US-09-623-618B-22	Sequence 22, Appl
29	59.5	49.2	31	4	US-09-623-618B-13	Sequence 13, Appl
30	57.5	47.5	30	4	US-09-623-618B-21	Sequence 21, Appl
31	57.5	47.5	31	4	US-09-623-618B-20	Sequence 20, Appl
32	41	33.9	516	4	US-09-154-750A-86	Sequence 86, Appl
33	41	33.9	589	2	US-08-317-305-2	Sequence 2, Appli
34	41	33.9	589	2	US-08-317-305-4	Sequence 4, Appli
35	41	33.9	589	3	US-08-862-508-2	Sequence 2, Appli
36	41	33.9	589	3	US-08-862-508-4	Sequence 4, Appli
37	41	33.9	589	5	PCT-US95-12508-2	Sequence 2, Appli
38	41	33.9	589	5	PCT-US95-12508-4	Sequence 4, Appli
39	39	32.2	341	1	US-08-062-024B-5	Sequence 5, Appli
40	39	32.2	341	1	US-08-891-254-5	Sequence 5, Appli
41	39	32.2	341	2	US-08-756-407-5	Sequence 5, Appli
42	39	32.2	341	2	US-08-819-539-5	Sequence 5, Appli
43	39	32.2	341	2	US-09-030-270A-5	Sequence 5, Appli
44	39	32.2	341	4	US-08-984-207-5	Sequence 5, Appli
45	39	32.2	341	4	US-09-013-587-5	Sequence 5, Appli

ALIGNMENTS

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RESULT 1
US-08-066-480-1
; Sequence 1, Application US/08066480
; Patent No. 5424286
; GENERAL INFORMATION:
;   APPLICANT:  Eng, John
;   TITLE OF INVENTION:  Pharmaceutical Compositions And Use of
;   TITLE OF INVENTION:  Exendin-3 and Exendin-4 for Treatment of Diabetes Mellitus
;   NUMBER OF SEQUENCES:  7
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Allegretti & Witcoff, Ltd.
;     STREET:  10 S. Wacker Drive
;     CITY:  Chicago
;     STATE:  Illinois
;     COUNTRY:  USA
;     ZIP:  60606
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/066,480
;     FILING DATE:  24-MAR-1993
;     CLASSIFICATION:  514
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  McDonnell, John J
;     REGISTRATION NUMBER:  26,949
;     REFERENCE/DOCKET NUMBER:  93,084
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  312-715-1000
;     TELEFAX:  312-715-1234
; INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  39 amino acids
;     TYPE:  amino acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
;   FEATURE:
;     NAME/KEY:  Peptide
;     LOCATION:  1..39
;     OTHER INFORMATION:  /label= Exendin-3
US-08-066-480-1

  Query Match           75.2%;  Score 91;  DB 1;  Length 39;
  Best Local Similarity  65.6%;  Pred. No. 8.7e-10;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (31)
; OTHER INFORMATION: tPro
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (36)
; OTHER INFORMATION: tPro
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (37)
; OTHER INFORMATION: tPro
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (38)
; OTHER INFORMATION: tPro
; FEATURE:
; OTHER INFORMATION: c-term amidation
US-09-756-690A-36

Query Match 76.9%; Score 93; DB 9; Length 39;
Best Local Similarity 68.8%; Pred. No. 1.7e-09;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
|| ||| ||||||| ||||||||||
Db 4 GTFTSDLSKQLEEEAVRLFIEFLKNGGXSSGA 35

RESULT 15
US-09-756-690A-39
; Sequence 39, Application US/09756690A
; Publication No. US20030036504A1
; GENERAL INFORMATION:
; APPLICANT: KOLTERMAN, ORVILLE G.
; APPLICANT: YOUNG, ANDREW A.
; TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF
; TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
; FILE REFERENCE: 249/124
; CURRENT APPLICATION NUMBER: US/09/756,690A
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/175,365
; PRIOR FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 188
; SOFTWARE: PatentIn Ver 2.1
; SEQ ID NO 39
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (31)
; OTHER INFORMATION: MeAla
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (36)
; OTHER INFORMATION: MeAla
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (37)
; OTHER INFORMATION: MeAla
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (38)
; OTHER INFORMATION: MeAla
; FEATURE:
; OTHER INFORMATION: c-term amidation
US-09-756-690A-39

Query Match 76.9%; Score 93; DB 9; Length 39;
Best Local Similarity 68.8%; Pred. No. 1.7e-09;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
|| ||| ||||||| ||||||||||
Db 4 GTFTSDLSKQLEEEAVRLFIEFLKNGGXSSGA 35

Search completed: June 24, 2003, 23:20:26
Job time : 30.5 secs

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;  EARLIER FILING DATE: 1997-11-14
;  EARLIER APPLICATION NUMBER: US 60/066,029
;  EARLIER FILING DATE: 1997-11-14
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 99
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificially synthesized sequence of novel exendin agonist
;   OTHER INFORMATION: compound
;   FEATURE:
;   OTHER INFORMATION: Xaa in positions 31, 36 and 37 stands for homoproline.
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (37)...(37)
;   OTHER INFORMATION: amidated hPro (homoprolinamide)
US-09-003-869-99

  Query Match             76.9%;  Score 93;  DB 10;  Length 37;
  Best Local Similarity   68.8%;  Pred. No. 1.6e-09;
  Matches   22;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||||||||
Db          4 GTFTSDASKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 12
US-09-003-869-183
; Sequence 183, Application US/09003869A
; Patent No. US20020137666A1
; GENERAL INFORMATION:
;  APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
;  APPLICANT: PRICKETT, KATHRYN S.
;  APPLICANT: BHAVSAR, SUNIL
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
;  TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
;  FILE REFERENCE: 231/181
;  CURRENT APPLICATION NUMBER: US/09/003,869A
;  CURRENT FILING DATE: 1998-01-07
;  EARLIER APPLICATION NUMBER: US 60/034,905
;  EARLIER FILING DATE: 1997-01-07
;  EARLIER APPLICATION NUMBER: US 60/055,404
;  EARLIER FILING DATE: 1997-08-08
;  EARLIER APPLICATION NUMBER: US 60/065,442
;  EARLIER FILING DATE: 1997-11-14
;  EARLIER APPLICATION NUMBER: US 60/066,029
;  EARLIER FILING DATE: 1997-11-14
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 183
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificially synthesized sequence of novel exendin agonist
;   OTHER INFORMATION: compound
;   FEATURE:
;   OTHER INFORMATION: Xaa in positions 31, 36 and 37 stands for n-methylalanine.
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (37)...(37)
;   OTHER INFORMATION: amidated Nmeala (n-methylalaninamide)
US-09-003-869-183

  Query Match             76.9%;  Score 93;  DB 10;  Length 37;
  Best Local Similarity   68.8%;  Pred. No. 1.6e-09;
  Matches   22;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||||||||
Db          4 GTFTSALSKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 13
US-09-756-690A-35
; Sequence 35, Application US/09756690A
; Publication No. US20030036504A1
; GENERAL INFORMATION:
;  APPLICANT: KOLTERMAN, ORVILLE G.
;  APPLICANT:  YOUNG, ANDREW A.
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF
;  TITLE OF INVENTION:  TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
;  FILE REFERENCE: 249/124
;  CURRENT APPLICATION NUMBER: US/09/756,690A
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: PatentIn Ver 2.1
; SEQ ID NO 35
;   LENGTH: 39
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (31)
;   OTHER INFORMATION: tPro
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (36)
;   OTHER INFORMATION: tPro
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (37)
;   OTHER INFORMATION: tPro
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (38)
;   OTHER INFORMATION: tPro
;   FEATURE:
;   OTHER INFORMATION: c-term amidation
US-09-756-690A-35

  Query Match             76.9%;  Score 93;  DB 9;  Length 39;
  Best Local Similarity   68.8%;  Pred. No. 1.7e-09;
  Matches   22;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||||||||
Db          4 GTFTSDLSKQLEEEAVRLFIEFLKNGGXSSGA 35


RESULT 14
US-09-756-690A-36
; Sequence 36, Application US/09756690A
; Publication No. US20030036504A1
; GENERAL INFORMATION:
;  APPLICANT: KOLTERMAN, ORVILLE G.
;  APPLICANT:  YOUNG, ANDREW A.
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF
;  TITLE OF INVENTION:  TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
;  FILE REFERENCE: 249/124
;  CURRENT APPLICATION NUMBER: US/09/756,690A
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: PatentIn Ver 2.1
; SEQ ID NO 36
;   LENGTH: 39
;   TYPE: PRT
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; SEQ ID NO 183
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
;   FEATURE:
;   OTHER INFORMATION: c-term amidation
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (31)
;   OTHER INFORMATION: N-methylalanine
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (36)..(37)
;   OTHER INFORMATION: N-methylalanine
US-10-157-224A-183

  Query Match             76.9%;  Score 93;  DB 9;  Length 37;
  Best Local Similarity   68.8%;  Pred. No. 1.6e-09;
  Matches   22;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||||||||
Db          4 GTFTSALSKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 9
US-10-187-051-99
; Sequence 99, Application US/10187051
; Publication No. US20030087821A1
; GENERAL INFORMATION:
;  APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
;  APPLICANT:  PRICKETT, KATHRYN S.
;  APPLICANT:  BHAVSAR, SUNIL
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
;  TITLE OF INVENTION:  THE REDUCTION OF FOOD INTAKE
;  FILE REFERENCE: 231/181
;  CURRENT APPLICATION NUMBER: US/10/187,051
;  CURRENT FILING DATE:  2002-06-28
;  PRIOR APPLICATION NUMBER: US/09/003,869
;  PRIOR FILING DATE: 1998-01-07
;  PRIOR APPLICATION NUMBER: US 60/034,905
;  PRIOR FILING DATE: 1997-01-07
;  PRIOR APPLICATION NUMBER: US 60/055,404
;  PRIOR FILING DATE: 1997-08-08
;  PRIOR APPLICATION NUMBER: US 60/065,442
;  PRIOR FILING DATE: 1997-11-14
;  PRIOR APPLICATION NUMBER: US 60/066,029
;  PRIOR FILING DATE: 1997-11-14
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 99
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificially synthesized sequence of novel exendin
;   OTHER INFORMATION: agonist
;   OTHER INFORMATION: compound
;   FEATURE:
;   OTHER INFORMATION: Xaa in positions 31, 36 and 37 stands for homoproline.
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (37)...(37)
;   OTHER INFORMATION: amidated hPro (homoprolinamide)
US-10-187-051-99

  Query Match             76.9%;  Score 93;  DB 9;  Length 37;
  Best Local Similarity   68.8%;  Pred. No. 1.6e-09;
  Matches   22;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||||||||
Db          4 GTFTSDASKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 10
US-10-187-051-183
; Sequence 183, Application US/10187051
; Publication No. US20030087821A1
; GENERAL INFORMATION:
;  APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
;  APPLICANT:  PRICKETT, KATHRYN S.
;  APPLICANT:  BHAVSAR, SUNIL
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
;  TITLE OF INVENTION:  THE REDUCTION OF FOOD INTAKE
;  FILE REFERENCE: 231/181
;  CURRENT APPLICATION NUMBER: US/10/187,051
;  CURRENT FILING DATE:  2002-06-28
;  PRIOR APPLICATION NUMBER: US/09/003,869
;  PRIOR FILING DATE: 1998-01-07
;  PRIOR APPLICATION NUMBER: US 60/034,905
;  PRIOR FILING DATE: 1997-01-07
;  PRIOR APPLICATION NUMBER: US 60/055,404
;  PRIOR FILING DATE: 1997-08-08
;  PRIOR APPLICATION NUMBER: US 60/065,442
;  PRIOR FILING DATE: 1997-11-14
;  PRIOR APPLICATION NUMBER: US 60/066,029
;  PRIOR FILING DATE: 1997-11-14
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 183
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificially synthesized sequence of novel exendin
;   OTHER INFORMATION: agonist
;   OTHER INFORMATION: compound
;   FEATURE:
;   OTHER INFORMATION: Xaa in positions 31, 36 and 37 stands for n-
;   OTHER INFORMATION: methylalanine.
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (37)...(37)
;   OTHER INFORMATION: amidated Nmeala (n-methylalaninamide)
US-10-187-051-183

  Query Match             76.9%;  Score 93;  DB 9;  Length 37;
  Best Local Similarity   68.8%;  Pred. No. 1.6e-09;
  Matches   22;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||||||||
Db          4 GTFTSALSKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 11
US-09-003-869-99
; Sequence 99, Application US/09003869A
; Patent No. US20020137666A1
; GENERAL INFORMATION:
;  APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
;  APPLICANT: PRICKETT, KATHRYN S.
;  APPLICANT: BHAVSAR, SUNIL
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
;  TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
;  FILE REFERENCE: 231/181
;  CURRENT APPLICATION NUMBER: US/09/003,869A
;  CURRENT FILING DATE: 1998-01-07
;  EARLIER APPLICATION NUMBER: US 60/034,905
;  EARLIER FILING DATE: 1997-01-07
;  EARLIER APPLICATION NUMBER: US 60/055,404
;  EARLIER FILING DATE: 1997-08-08
;  EARLIER APPLICATION NUMBER: US 60/065,442
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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (31)
;   OTHER INFORMATION: hPro
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (36)
;   OTHER INFORMATION: hPro
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (37)
;   OTHER INFORMATION: hPro
;   FEATURE:
;   OTHER INFORMATION: c-term amidation
US-09-756-690A-99

  Query Match             76.9%;  Score 93;  DB 9;  Length 37;
  Best Local Similarity   68.8%;  Pred. No. 1.6e-09;
  Matches   22;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||||||||
Db          4 GTFTSDASKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 6
US-09-756-690A-183
; Sequence 183, Application US/09756690A
; Publication No. US20030036504A1
; GENERAL INFORMATION:
;  APPLICANT: KOLTERMAN, ORVILLE G.
;  APPLICANT:  YOUNG, ANDREW A.
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF
;  TITLE OF INVENTION:  TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
;  FILE REFERENCE: 249/124
;  CURRENT APPLICATION NUMBER: US/09/756,690A
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: PatentIn Ver 2.1
; SEQ ID NO 183
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (31)
;   OTHER INFORMATION: NMeala
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (36)
;   OTHER INFORMATION: NMeala
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (37)
;   OTHER INFORMATION: NMeala
;   FEATURE:
;   OTHER INFORMATION: c-term amidation
US-09-756-690A-183

  Query Match             76.9%;  Score 93;  DB 9;  Length 37;
  Best Local Similarity   68.8%;  Pred. No. 1.6e-09;
  Matches   22;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||||||||
Db          4 GTFTSALSKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 7
US-10-157-224A-99
; Sequence 99, Application US/10157224A
; Publication No. US20030087820A1
; GENERAL INFORMATION:
;  APPLICANT: YOUNG, ANDREW A.
;  APPLICANT:  KOLTERMAN, ORVILLE G.
;  TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
;  TITLE OF INVENTION:  ADMINISTRATION THEREOF
;  FILE REFERENCE: 02001-050
;  CURRENT APPLICATION NUMBER: US/10/157,224A
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: 09/889,330
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: PCT/US00/00902
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 60/116,380
;  PRIOR FILING DATE: 1999-01-14
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
;   FEATURE:
;   OTHER INFORMATION: c-term amidation
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (31)
;   OTHER INFORMATION: Homoproline
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (36)..(37)
;   OTHER INFORMATION: Homoproline
US-10-157-224A-99

  Query Match             76.9%;  Score 93;  DB 9;  Length 37;
  Best Local Similarity   68.8%;  Pred. No. 1.6e-09;
  Matches   22;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||||||||
Db          4 GTFTSDASKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 8
US-10-157-224A-183
; Sequence 183, Application US/10157224A
; Publication No. US20030087820A1
; GENERAL INFORMATION:
;  APPLICANT: YOUNG, ANDREW A.
;  APPLICANT:  KOLTERMAN, ORVILLE G.
;  TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
;  TITLE OF INVENTION:  ADMINISTRATION THEREOF
;  FILE REFERENCE: 02001-050
;  CURRENT APPLICATION NUMBER: US/10/157,224A
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: 09/889,330
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: PCT/US00/00902
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 60/116,380
;  PRIOR FILING DATE: 1999-01-14
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: PatentIn Ver. 2.1
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;  TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
;  TITLE OF INVENTION:  ADMINISTRATION THEREOF
;  FILE REFERENCE: 02001-050
;  CURRENT APPLICATION NUMBER: US/10/157,224A
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: 09/889,330
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: PCT/US00/00902
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 60/116,380
;  PRIOR FILING DATE: 1999-01-14
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 171
;    LENGTH: 36
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
;    FEATURE:
;    OTHER INFORMATION: c-term amidation
US-10-157-224A-171

  Query Match             76.9%;  Score 93;  DB 9;  Length 36;
  Best Local Similarity   65.6%;  Pred. No. 1.6e-09;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||| ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 3
US-10-187-051-171
; Sequence 171, Application US/10187051
; Publication No. US20030087821A1
; GENERAL INFORMATION:
;  APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
;  APPLICANT:  PRICKETT, KATHRYN S.
;  APPLICANT:  BHAVSAR, SUNIL
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
;  TITLE OF INVENTION:  THE REDUCTION OF FOOD INTAKE
;  FILE REFERENCE: 231/181
;  CURRENT APPLICATION NUMBER: US/10/187,051
;  CURRENT FILING DATE:  2002-06-28
;  PRIOR APPLICATION NUMBER: US/09/003,869
;  PRIOR FILING DATE: 1998-01-07
;  PRIOR APPLICATION NUMBER: US 60/034,905
;  PRIOR FILING DATE: 1997-01-07
;  PRIOR APPLICATION NUMBER: US 60/055,404
;  PRIOR FILING DATE: 1997-08-08
;  PRIOR APPLICATION NUMBER: US 60/065,442
;  PRIOR FILING DATE: 1997-11-14
;  PRIOR APPLICATION NUMBER: US 60/066,029
;  PRIOR FILING DATE: 1997-11-14
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 171
;    LENGTH: 36
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: artificially synthesized sequence of novel exendin
;    OTHER INFORMATION: agonist
;    OTHER INFORMATION: compound
;    FEATURE:
;    NAME/KEY: AMIDATION
;    LOCATION: (36)...(36)
;    OTHER INFORMATION: amidated Pro (Prolinamide)
US-10-187-051-171

  Query Match             76.9%;  Score 93;  DB 9;  Length 36;
  Best Local Similarity   65.6%;  Pred. No. 1.6e-09;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||| ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 4
US-09-003-869-171
; Sequence 171, Application US/09003869A
; Patent No. US20020137666A1
; GENERAL INFORMATION:
;  APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
;  APPLICANT: PRICKETT, KATHRYN S.
;  APPLICANT: BHAVSAR, SUNIL
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
;  TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
;  FILE REFERENCE: 231/181
;  CURRENT APPLICATION NUMBER: US/09/003,869A
;  CURRENT FILING DATE: 1998-01-07
;  EARLIER APPLICATION NUMBER: US 60/034,905
;  EARLIER FILING DATE: 1997-01-07
;  EARLIER APPLICATION NUMBER: US 60/055,404
;  EARLIER FILING DATE: 1997-08-08
;  EARLIER APPLICATION NUMBER: US 60/065,442
;  EARLIER FILING DATE: 1997-11-14
;  EARLIER APPLICATION NUMBER: US 60/066,029
;  EARLIER FILING DATE: 1997-11-14
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 171
;    LENGTH: 36
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: artificially synthesized sequence of novel exendin agonist
;    OTHER INFORMATION: compound
;    FEATURE:
;    NAME/KEY: AMIDATION
;    LOCATION: (36)...(36)
;    OTHER INFORMATION: amidated Pro (Prolinamide)
US-09-003-869-171

  Query Match             76.9%;  Score 93;  DB 10;  Length 36;
  Best Local Similarity   65.6%;  Pred. No. 1.6e-09;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||| ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 5
US-09-756-690A-99
; Sequence 99, Application US/09756690A
; Publication No. US20030036504A1
; GENERAL INFORMATION:
;  APPLICANT: KOLTERMAN, ORVILLE G.
;  APPLICANT:  YOUNG, ANDREW A.
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF
;  TITLE OF INVENTION:  TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
;  FILE REFERENCE: 249/124
;  CURRENT APPLICATION NUMBER: US/09/756,690A
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: PatentIn Ver 2.1
; SEQ ID NO 99
;    LENGTH: 37
;    TYPE: PRT
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 24, 2003, 23:07:45 ; Search time 30.5 Seconds
(without alignments)
141.911 Million cell updates/sec

Title: US-09-889-331A-47
Perfect score: 121
Sequence: 1 XXXGTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGAXXXXX 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	93	76.9	36	9	US-09-756-690A-171	Sequence 171, App
2	93	76.9	36	9	US-10-157-224A-171	Sequence 171, App
3	93	76.9	36	9	US-10-187-051-171	Sequence 171, App
4	93	76.9	36	10	US-09-003-869-171	Sequence 171, App
5	93	76.9	37	9	US-09-756-690A-99	Sequence 99, Appl
6	93	76.9	37	9	US-09-756-690A-183	Sequence 183, App
7	93	76.9	37	9	US-10-157-224A-99	Sequence 99, Appl
8	93	76.9	37	9	US-10-157-224A-183	Sequence 183, App
9	93	76.9	37	9	US-10-187-051-99	Sequence 99, Appl
10	93	76.9	37	9	US-10-187-051-183	Sequence 183, App
11	93	76.9	37	10	US-09-003-869-99	Sequence 99, Appl
12	93	76.9	37	10	US-09-003-869-183	Sequence 183, App
13	93	76.9	39	9	US-09-756-690A-35	Sequence 35, Appl
14	93	76.9	39	9	US-09-756-690A-36	Sequence 36, Appl
15	93	76.9	39	9	US-09-756-690A-39	Sequence 39, Appl
16	93	76.9	39	9	US-10-157-224A-35	Sequence 35, Appl
17	93	76.9	39	9	US-10-157-224A-36	Sequence 36, Appl
18	93	76.9	39	9	US-10-157-224A-39	Sequence 39, Appl
19	93	76.9	39	9	US-10-187-051-35	Sequence 35, Appl
20	93	76.9	39	9	US-10-187-051-36	Sequence 36, Appl
21	93	76.9	39	9	US-10-187-051-39	Sequence 39, Appl
22	93	76.9	39	10	US-09-003-869-35	Sequence 35, Appl
23	93	76.9	39	10	US-09-003-869-36	Sequence 36, Appl
24	93	76.9	39	10	US-09-003-869-39	Sequence 39, Appl
25	92	76.0	35	9	US-09-756-690A-69	Sequence 69, Appl
26	92	76.0	35	9	US-09-756-690A-173	Sequence 173, App
27	92	76.0	35	9	US-10-157-224A-69	Sequence 69, Appl
28	92	76.0	35	9	US-10-157-224A-173	Sequence 173, App
29	92	76.0	35	9	US-10-187-051-69	Sequence 69, Appl
30	92	76.0	35	9	US-10-187-051-173	Sequence 173, App
31	92	76.0	35	10	US-09-003-869-69	Sequence 69, Appl
32	92	76.0	35	10	US-09-003-869-173	Sequence 173, App
33	92	76.0	36	9	US-09-756-690A-67	Sequence 67, Appl
34	92	76.0	36	9	US-09-756-690A-86	Sequence 86, Appl
35	92	76.0	36	9	US-09-756-690A-170	Sequence 170, App
36	92	76.0	36	9	US-09-756-690A-184	Sequence 184, App
37	92	76.0	36	9	US-10-157-224A-67	Sequence 67, Appl
38	92	76.0	36	9	US-10-157-224A-86	Sequence 86, Appl
39	92	76.0	36	9	US-10-157-224A-170	Sequence 170, App
40	92	76.0	36	9	US-10-157-224A-184	Sequence 184, App
41	92	76.0	36	9	US-10-187-051-67	Sequence 67, Appl
42	92	76.0	36	9	US-10-187-051-86	Sequence 86, Appl
43	92	76.0	36	9	US-10-187-051-170	Sequence 170, App
44	92	76.0	36	9	US-10-187-051-184	Sequence 184, App
45	92	76.0	36	10	US-09-003-869-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1
US-09-756-690A-171
; Sequence 171, Application US/09756690A
; Publication No. US20030036504A1
; GENERAL INFORMATION:
; APPLICANT: KOLTERMAN, ORVILLE G.
; APPLICANT: YOUNG, ANDREW A.
; TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF
; TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
; FILE REFERENCE: 249/124
; CURRENT APPLICATION NUMBER: US/09/756,690A
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/175,365
; PRIOR FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 188
; SOFTWARE: PatentIn Ver 2.1
; SEQ ID NO 171
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
; FEATURE:
; OTHER INFORMATION: c-term amidation
US-09-756-690A-171

Query Match 76.9%; Score 93; DB 9; Length 36;
Best Local Similarity 65.6%; Pred. No. 1.6e-09;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| ||||||    ||||| ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35
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RESULT 2
US-10-157-224A-171
; Sequence 171, Application US/10157224A
; Publication No. US20030087820A1
; GENERAL INFORMATION:
; APPLICANT: YOUNG, ANDREW A.
; APPLICANT: KOLTERMAN, ORVILLE G.

A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85876
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-310 <STO>
A;Cross-references: GB:AE005174; NID:g12516714; PIDN:AAG57475.1; GSPDB:GN00145; UWGP:Z36
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: yfdC

Query Match 33.9%; Score 38; DB 2; Length 310;
Best Local Similarity 34.8%; Pred. No. 19;
Matches 8; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 12 KQXEEEAVRLXXXXLXGGXSSGA 34
|: | :|: | : | | ||
Db 50 KELERDAMALLWSAIAAGLSMGA 72

RESULT 13
A65008
hypothetical 34.5 kD protein in argW 5'region - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: A65008
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: A65008
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-310 <BLAT>
A;Cross-references: GB:AE000323; GB:U00096; NID:g1788684; PIDN:AAC75407.1; PID:g1788689;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: yfdC

Query Match 33.9%; Score 38; DB 2; Length 310;
Best Local Similarity 34.8%; Pred. No. 19;
Matches 8; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 12 KQXEEEAVRLXXXXLXGGXSSGA 34
|: | :|: | : | | ||
Db 50 KELERDAMALLWSAIAAGLSMGA 72

RESULT 14
AG0805
probable membrane protein STY2625 [imported] - Salmonella enterica subsp. enterica serov
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: AG0805
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:11677608
A;Accession: AG0805
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-313 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD07625.1; PID:g16503616; GSPDB:GN00176
C;Genetics:
A;Gene: STY2625

Query Match 33.9%; Score 38; DB 2; Length 313;
Best Local Similarity 34.8%; Pred. No. 20;
Matches 8; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 12 KQXEEEAVRLXXXXLXGGXSSGA 34
|: | :|: | : | | ||
Db 53 KEMERDAMALLWSAIAAGLSMGA 75

RESULT 15
AI3286
transcription regulator [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AI3286
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melit
A;Reference number: AD3252; PMID:11756688
A;Accession: AI3286
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-207 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL51460.1; PID:g17982170; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI0279
A;Map position: I

Query Match 33.0%; Score 37; DB 2; Length 207;
Best Local Similarity 43.5%; Pred. No. 20;
Matches 10; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

Qy 11 SKQXEEEAVRLXXXXLXGGXSSG 33
:| | ||||| | | |
Db 171 NKLSETEAVRLIEVNLAKGPKRG 193

Search completed: June 24, 2003, 23:08:35
Job time : 26 secs

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F;350/Binding site: heme iron (Cys) (axial ligand) #status predicted

  Query Match           34.8%;  Score 39;  DB 1;  Length 401;
  Best Local Similarity  47.6%;  Pred. No. 16;
  Matches   10;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLXGGXSS 32
              |  ||||| |    |  |  |
Db        221 KASEEEAVGLAAGMLVAGHES 241


RESULT 8
F86457
unknown protein, 33246-28649 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: F86457
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: F86457
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-781 <STO>
A;Cross-references: GB:AE005172; NID:g10645506; PIDN:AAG21618.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1

  Query Match           34.8%;  Score 39;  DB 2;  Length 781;
  Best Local Similarity  50.0%;  Pred. No. 32;
  Matches    9;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         17 EAVRLXXXXLXGGXSSGA 34
              | |:|    |  | ||||
Db        722 EMVKLASIQLASGDSSGA 739


RESULT 9
T51087
chloroplast FtsZ-like protein [imported] - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
C;Accession: T51087
R;El-Shami, M.; Alcaraz, J.P.; Lerbs-Mache, S.; Falconet, D.
submitted to the EMBL Data Library, February 2000
A;Description: A new cDNA encoding FtsZ-like protein from Nicotiana tabacum.
A;Reference number: Z25288
A;Accession: T51087
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-468 <ELS>
A;Cross-references: EMBL:AJ271750; PIDN:CAB89288.1
A;Experimental source: variety Bright Yellow 2
C;Genetics:
A;Gene: ftsZ
C;Superfamily: cell division protein ftsZ
C;Keywords: chloroplast

  Query Match           34.4%;  Score 38.5;  DB 2;  Length 468;
  Best Local Similarity  33.3%;  Pred. No. 24;
  Matches   12;  Conservative    2;  Mismatches   17;  Indels    5;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVR-----LXXXXLXGGXSSGA 34
              |      |||  ||||          : ||  :||
Db        176 GMNAANESKQAIEEAVYGADMVFVTAGMGGGTGTGA 211


RESULT 10
D71137
probable transcription initiation factor IIB - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C;Accession: D71137
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophili
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: D71137
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-208 <KAW>
A;Cross-references: GB:AP000003; NID:g3236130; PIDN:BAA29958.1; PID:g3257275
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBa
C;Genetics:
A;Gene: PH0864
C;Superfamily: transcription initiation factor IIB; transcription initiation factor I
C;Keywords: transcription initiation

  Query Match           33.9%;  Score 38;  DB 2;  Length 208;
  Best Local Similarity  36.4%;  Pred. No. 13;
  Matches    8;  Conservative    3;  Mismatches   11;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLXGGXSSG 33
              |  | ||||:    :  | : |
Db         38 KHVEREAVRIYRKLIKSGVTKG 59


RESULT 11
F91032
probable transport ECs3230 [imported] - Escherichia coli (strain O157:H7, substrain R
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: F91032
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F91032
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-310 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB36653.1; PID:g13362700; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs3230

  Query Match           33.9%;  Score 38;  DB 2;  Length 310;
  Best Local Similarity  34.8%;  Pred. No. 19;
  Matches    8;  Conservative    4;  Mismatches   11;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLXGGXSSGA 34
              |: | :|: |    :  | | ||
Db         50 KELERDAMALLWSAIAAGLSMGA 72


RESULT 12
G85876
probable transport yfdC [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: G85876
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
```

```
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 3
T51089
plastid division protein ftsZ1 [imported] - moss (Physcomitrella patens)
C;Species: Physcomitrella patens
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
C;Accession: T51089
R;Kruse, S.; Kiessling, J.; Harter, K.; Rensing, S.; Decker, E.; Reski, R.
submitted to the EMBL Data Library, August 1999
A;Description: Two distinct nuclear-encoded plant ftsZ-genes are highly conserved, both
A;Reference number: Z25290
A;Accession: T51089
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-458 <KRU>
A;Cross-references: EMBL:AJ249138; PIDN:CAB54558.1
C;Genetics:
A;Gene: ftsZ
A;Introns: 193/3; 293/3; 324/1; 365/3; 396/3; 418/3
C;Superfamily: cell division protein ftsZ
C;Keywords: chloroplast

  Query Match             36.2%;  Score 40.5;  DB 2;  Length 458;
  Best Local Similarity   33.3%;  Pred. No. 9.7;
  Matches   12;  Conservative    2;  Mismatches   17;  Indels    5;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVR-----LXXXXLXGGXSSGA 34
              |      ||   |||:|          : ||  |||
Db        169 GCSAAEESKAMVEEALRGADMVFVTAGMGGGTGSGA 204


RESULT 4
T51090
plastid division protein ftsZ2 [imported] - moss (Physcomitrella patens)
C;Species: Physcomitrella patens
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
C;Accession: T51090
R;Kruse, S.; Kiessling, J.; Harter, K.; Rensing, S.; Decker, E.; Reski, R.
submitted to the EMBL Data Library, August 1999
A;Description: Two distinct nuclear-encoded plant ftsZ-genes are highly conserved, both
A;Reference number: Z25290
A;Accession: T51090
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-464 <KRU>
A;Cross-references: EMBL:AJ249139; PIDN:CAB76386.1
C;Genetics:
A;Gene: ftsZ
A;Introns: 201/3; 301/3; 332/1; 373/3; 404/3; 426/3
C;Superfamily: cell division protein ftsZ
C;Keywords: chloroplast

  Query Match             36.2%;  Score 40.5;  DB 2;  Length 464;
  Best Local Similarity   33.3%;  Pred. No. 9.8;
  Matches   12;  Conservative    2;  Mismatches   17;  Indels    5;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVR-----LXXXXLXGGXSSGA 34
              |      ||   |||:|          : ||  |||
Db        177 GCSAAEESKAMVEEALRGADMVFVTAGMGGGTGSGA 212


RESULT 5
G97690
hypothetical protein AGR_C_5013 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Accession: G97690
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; PMID:11743194
A;Accession: G97690
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-189 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK88480.1; PID:g15157987; GSPDB:GN00169
C;Genetics:
A;Gene: AGR_C_5013
A;Map position: circular chromosome

  Query Match             34.8%;  Score 39;  DB 2;  Length 189;
  Best Local Similarity   43.5%;  Pred. No. 7.5;
  Matches   10;  Conservative    1;  Mismatches   12;  Indels    0;  Gaps    0;

Qy         11 SKQXEEEAVRLXXXXLXGGXSSG 33
              :|  | |||||    |  |   |
Db        154 NKMSETEAVRLVEVNLAKGPKRG 176


RESULT 6
AD2916
transcription regulator, CarD family Atu2765 [imported] - Agrobacterium tumefaciens (
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AD2916
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AD2916
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-189 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL43746.1; PID:g17741280; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu2765
A;Map position: circular chromosome

  Query Match             34.8%;  Score 39;  DB 2;  Length 189;
  Best Local Similarity   43.5%;  Pred. No. 7.5;
  Matches   10;  Conservative    1;  Mismatches   12;  Indels    0;  Gaps    0;

Qy         11 SKQXEEEAVRLXXXXLXGGXSSG 33
              :|  | |||||    |  |   |
Db        154 NKMSETEAVRLVEVNLAKGPKRG 176


RESULT 7
I40208
cytochrome P450 BJ-1 CYP112 - Bradyrhizobium japonicum
N;Contains: oxidoreductase (EC 1.-.-.-)
C;Species: Bradyrhizobium japonicum
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Mar-2000
C;Accession: I40208
R;Tully, R.E.; Keister, D.L.
Appl. Environ. Microbiol. 59, 4136-4142, 1993
A;Title: Cloning and mutagenesis of a cytochrome P-450 locus from Bradyrhizobium japo
A;Reference number: I40207
A;Accession: I40208
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-401 <RES>
A;Cross-references: EMBL:U12678; NID:g529961; PIDN:AAC28889.1; PID:g529962
C;Genetics:
A;Gene: CYP112
C;Superfamily: Bacillus cytochrome P450 CYP106; cytochrome P450 homology
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;234-372/Domain: cytochrome P450 homology <CYP>
```

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OM protein - protein search, using sw model

Run on: June 24, 2003, 23:03:10 ; Search time 25 Seconds
(without alignments)
153.815 Million cell updates/sec

Title: US-09-889-331A-48
Perfect score: 112
Sequence: 1 XXXGTXXXXXSKQXEEEAVRLXXXXLXGGXSSGAXXXXXX 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	68.5	61.2	39	1	HWGH3Z	exendin-3 - Mexica
2	68.5	61.2	39	1	HWGH4G	exendin-4 - Gila m
3	40.5	36.2	458	2	T51089	plastid division p
4	40.5	36.2	464	2	T51090	plastid division p
5	39	34.8	189	2	G97690	hypothetical prote
6	39	34.8	189	2	AD2916	transcription regu
7	39	34.8	401	1	I40208	cytochrome P450 BJ
8	39	34.8	781	2	F86457	unknown protein, 3
9	38.5	34.4	468	2	T51087	chloroplast FtsZ-l
10	38	33.9	208	2	D71137	probable transcrip
11	38	33.9	310	2	F91032	probable transport
12	38	33.9	310	2	G85876	probable transport
13	38	33.9	310	2	A65008	hypothetical 34.5
14	38	33.9	313	2	AG0805	probable membrane
15	37	33.0	207	2	AI3286	transcription regu
16	37	33.0	248	2	A69173	conserved hypothet
17	37	33.0	328	2	T06215	glucan endo-1,3-be
18	37	33.0	356	2	H90168	GTP-binding protei
19	37	33.0	449	1	A41520	chromogranin A pre
20	37	33.0	536	2	S71332	natriuretic peptid
21	37	33.0	850	2	T13352	stn-A protein - fr
22	36.5	32.6	124	2	T36629	probable transcrip
23	36.5	32.6	456	2	S69070	hypothetical prote
24	36	32.1	144	2	E86303	hypothetical prote
25	36	32.1	249	2	C84185	hypothetical prote
26	36	32.1	251	2	S53321	cytochrome B561 -
27	36	32.1	284	2	JC6198	alpha-tropomyosin
28	36	32.1	344	2	D75311	conserved hypothet
29	36	32.1	402	2	A75054	molybdenum cofacto
30	36	32.1	472	2	A97067	thiamine biosynthe
31	36	32.1	784	2	S26638	SPR-1 protein - hu
32	36	32.1	823	2	A36378	probable transcrip
33	36	32.1	3068	1	A44062	genome polyprotein
34	35.5	31.7	382	1	I39848	cell division init
35	35	31.2	129	2	A44828	alkaline phosphata
36	35	31.2	281	2	S32566	actin-binding prot
37	35	31.2	300	2	E71023	probable transcrip
38	35	31.2	300	2	E75110	transcription init
39	35	31.2	338	2	G83508	flagellar motor sw
40	35	31.2	370	2	F86338	protein F2D10.2 [i
41	35	31.2	446	2	A75494	probable Na+/H+ an
42	35	31.2	563	2	A47153	iduronate-2-sulfat
43	35	31.2	803	2	C83561	probable type II s
44	35	31.2	925	2	T02811	DNA excision/repai
45	35	31.2	1029	2	AG3363	acriflavin resista

ALIGNMENTS

RESULT 1
HWGH3Z
exendin-3 - Mexican beaded lizard
C;Species: Heloderma horridum (Mexican beaded lizard)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 21-Nov-1997
C;Accession: A23674
R;Eng, J.; Andrews, P.C.; Kleinman, W.A.; Singh, L.; Raufman, J.P.
J. Biol. Chem. 265, 20259-20262, 1990
A;Title: Purification and structure of exendin-3, a new pancreatic secretagogue isola
A;Reference number: A23674; MUID:91056067; PMID:1700785
A;Accession: A23674
A;Molecule type: protein
A;Residues: 1-39 <ENG>
C;Comment: Exendins are venom components that are thought to bind to receptors for va
g in secretion of amylase.
C;Superfamily: glucagon
C;Keywords: amidated carboxyl end; duplication; secretagogue; venom
F;39/Modified site: amidated carboxyl end (Ser) #status experimental

Query Match 61.2%; Score 68.5; DB 1; Length 39;
Best Local Similarity 59.4%; Pred. No. 3.9e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

```
Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35
```

RESULT 2
HWGH4G
exendin-4 - Gila monster
C;Species: Heloderma suspectum (Gila monster)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 21-Nov-1997
C;Accession: A42486
R;Eng, J.; Kleinman, W.A.; Singh, L.; Singh, G.; Raufman, J.P.
J. Biol. Chem. 267, 7402-7405, 1992
A;Title: Isolation and characterization of exendin-4, an exendin-3 analogue, from Hel
A;Reference number: A42486; MUID:92218391; PMID:1313797
A;Accession: A42486
A;Molecule type: protein
A;Residues: 1-39 <ENG>
C;Comment: Exendin-4 does not stimulate amylase secretion by pancreatic acinar cells.
C;Superfamily: glucagon
C;Keywords: amidated carboxyl end; duplication; venom
F;39/Modified site: amidated carboxyl end (Ser) #status experimental

Query Match 61.2%; Score 68.5; DB 1; Length 39;
Best Local Similarity 59.4%; Pred. No. 3.9e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

```
Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
```

```
;  APPLICANT: Prickett, Kathryn S
;  APPLICANT:  Young, Andrew A
;  TITLE OF INVENTION: MODIFIED EXENDINS AND EXENDIN AGONISTS
;  FILE REFERENCE: 030639.0028.UTL(253/204)
;  CURRENT APPLICATION NUMBER: US/09/561,226A
;  CURRENT FILING DATE:  2000-04-28
;  PRIOR APPLICATION NUMBER: 60/132,018
;  PRIOR FILING DATE: 1999-04-30
;  NUMBER OF SEQ ID NOS: 240
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 86
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Amino Acid Sequence
;   NAME/KEY: VARIANT
;   LOCATION: 31, 36-37
;   OTHER INFORMATION: Xaa in positions 31, 36-37 stands for hPro
;   NAME/KEY: AMIDATION
;   LOCATION: 37
;   OTHER INFORMATION: hPro in position 37 is amidated
US-09-561-226A-86

  Query Match             76.9%;  Score 93;  DB 19;  Length 37;
  Best Local Similarity   68.8%;  Pred. No. 4.7e-09;
  Matches   22;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||||||||
Db          4 GTFTSDASKQMEEEAVRLFIEWLKNGGXSSGA 35


Search completed: June 24, 2003, 23:16:46
Job time : 222 secs
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;   OTHER INFORMATION: compound
;   FEATURE:
;   OTHER INFORMATION: Xaa in positions 31, 36 and 37 stands for homoproline.
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (37)...(37)
;   OTHER INFORMATION: amidated hPro (homoprolinamide)
US-09-003-869-99

  Query Match             76.9%;  Score 93;  DB 14;  Length 37;
  Best Local Similarity   68.8%;  Pred. No. 4.7e-09;
  Matches   22;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||||||||
Db          4 GTFTSDASKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 12
US-09-003-869-183
; Sequence 183, Application US/09003869A
; GENERAL INFORMATION:
;  APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
;  APPLICANT: PRICKETT, KATHRYN S.
;  APPLICANT: BHAVSAR, SUNIL
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
;  TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
;  FILE REFERENCE: 231/181
;  CURRENT APPLICATION NUMBER: US/09/003,869A
;  CURRENT FILING DATE: 1998-01-07
;  EARLIER APPLICATION NUMBER: US 60/034,905
;  EARLIER FILING DATE: 1997-01-07
;  EARLIER APPLICATION NUMBER: US 60/055,404
;  EARLIER FILING DATE: 1997-08-08
;  EARLIER APPLICATION NUMBER: US 60/065,442
;  EARLIER FILING DATE: 1997-11-14
;  EARLIER APPLICATION NUMBER: US 60/066,029
;  EARLIER FILING DATE: 1997-11-14
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 183
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificially synthesized sequence of novel exendin agonist
;   OTHER INFORMATION: compound
;   FEATURE:
;   OTHER INFORMATION: Xaa in positions 31, 36 and 37 stands for n-methylalanine.
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (37)...(37)
;   OTHER INFORMATION: amidated Nmeala (n-methylalaninamide)
US-09-003-869-183

  Query Match             76.9%;  Score 93;  DB 14;  Length 37;
  Best Local Similarity   68.8%;  Pred. No. 4.7e-09;
  Matches   22;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||||||||
Db          4 GTFTSALSKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 13
US-09-323-867A-99
; Sequence 99, Application US/09323867A
; GENERAL INFORMATION:
;  APPLICANT: Amylin Pharmaceuticals, Inc.
;  APPLICANT:  Young, Andrew et al.
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
;  TITLE OF INVENTION:  OF GESTATIONAL DIABETES MELLITUS
;  FILE REFERENCE: 030639.0032.UTL2 (243/131US)
;  CURRENT APPLICATION NUMBER: US/09/323,867A
;  CURRENT FILING DATE:  1999-06-01
;  NUMBER OF SEQ ID NOS: 189
;  SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 99
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificial sequence with specific variable residues
;   NAME/KEY: VARIANT
;   LOCATION: (31)
;   OTHER INFORMATION: Xaa is homoproline
;   NAME/KEY: VARIANT
;   LOCATION: (36)..(37)
;   OTHER INFORMATION: Xaa is homoproline
;   NAME/KEY: MOD_RES
;   LOCATION: (37)
;   OTHER INFORMATION: AMIDATION, Position 37 is homoproline-NH2
US-09-323-867A-99

  Query Match             76.9%;  Score 93;  DB 17;  Length 37;
  Best Local Similarity   68.8%;  Pred. No. 4.7e-09;
  Matches   22;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||||||||
Db          4 GTFTSDASKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 14
US-09-323-867A-183
; Sequence 183, Application US/09323867A
; GENERAL INFORMATION:
;  APPLICANT: Amylin Pharmaceuticals, Inc.
;  APPLICANT:  Young, Andrew et al.
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
;  TITLE OF INVENTION:  OF GESTATIONAL DIABETES MELLITUS
;  FILE REFERENCE: 030639.0032.UTL2 (243/131US)
;  CURRENT APPLICATION NUMBER: US/09/323,867A
;  CURRENT FILING DATE:  1999-06-01
;  NUMBER OF SEQ ID NOS: 189
;  SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 183
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificial sequence with specific variable residues
;   NAME/KEY: VARIANT
;   LOCATION: (31)
;   OTHER INFORMATION: Xaa is N-methylalanine
;   NAME/KEY: VARIANT
;   LOCATION: (36)..(37)
;   OTHER INFORMATION: Xaa is N-methylalanine
;   NAME/KEY: MOD_RES
;   LOCATION: (37)
;   OTHER INFORMATION: AMIDATION, Position 37 is N-methylalanine-NH2
US-09-323-867A-183

  Query Match             76.9%;  Score 93;  DB 17;  Length 37;
  Best Local Similarity   68.8%;  Pred. No. 4.7e-09;
  Matches   22;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||||||||
Db          4 GTFTSALSKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 15
US-09-561-226A-86
; Sequence 86, Application US/09561226A
; GENERAL INFORMATION:
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  Best Local Similarity   65.6%;  Pred. No. 4.5e-09;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||| ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 8
US-09-756-690A-171
; Sequence 171, Application US/09756690A
; GENERAL INFORMATION:
;  APPLICANT: KOLTERMAN, ORVILLE G.
;  APPLICANT:  YOUNG, ANDREW A.
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF
;  TITLE OF INVENTION:  TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
;  FILE REFERENCE: 249/124
;  CURRENT APPLICATION NUMBER: US/09/756,690A
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: PatentIn Ver 2.1
; SEQ ID NO 171
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
;   FEATURE:
;   OTHER INFORMATION: c-term amidation
US-09-756-690A-171

  Query Match             76.9%;  Score 93;  DB 21;  Length 36;
  Best Local Similarity   65.6%;  Pred. No. 4.5e-09;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||| ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 9
US-09-889-331-189
; Sequence 189, Application US/09889331
; GENERAL INFORMATION:
;  APPLICANT: YOUNG, ANDREW A.
;  APPLICANT:  GEDULIN, BRONISLAVA
;  TITLE OF INVENTION: METHODS FOR GLUCAGON SUPPRESSION
;  FILE REFERENCE: 030639.0031.UTL1 (249/167)
;  CURRENT APPLICATION NUMBER: US/09/889,331
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: PCT/US00/00942
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 60/116,380
;  PRIOR FILING DATE: 1999-01-14
;  PRIOR APPLICATION NUMBER: 60/132,017
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 239
;  SOFTWARE: FastSEQ for Windows Version 4.0, Microsoft WORD 97 SR-2
; SEQ ID NO 189
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Amino Acid Sequence
;   NAME/KEY: AMIDATION
;   LOCATION: (36)
;   OTHER INFORMATION: Pro in position 36 is amidated
US-09-889-331-189

  Query Match             76.9%;  Score 93;  DB 22;  Length 36;
  Best Local Similarity   65.6%;  Pred. No. 4.5e-09;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||| ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 10
US-09-554-531A-76
; Sequence 76, Application US/09554531A
; GENERAL INFORMATION:
;  APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
;  APPLICANT:  PRICKETT, KATHRYN S.
;  TITLE OF INVENTION: NOVEL EXENDIN AGONIST COMPOUNDS
;  FILE REFERENCE: 238/087 US
;  CURRENT APPLICATION NUMBER: US/09/554,531A
;  CURRENT FILING DATE:  2000-08-08
;  PRIOR APPLICATION NUMBER: PCT/US98/24273
;  PRIOR FILING DATE: 1998-11-13
;  PRIOR APPLICATION NUMBER: 60/066,029
;  PRIOR FILING DATE: 1997-11-14
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exendin agonist
;   FEATURE:
;   OTHER INFORMATION: c-term amidation
US-09-554-531A-76

  Query Match             76.9%;  Score 93;  DB 23;  Length 36;
  Best Local Similarity   65.6%;  Pred. No. 4.5e-09;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||| ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 11
US-09-003-869-99
; Sequence 99, Application US/09003869A
; GENERAL INFORMATION:
;  APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
;  APPLICANT: PRICKETT, KATHRYN S.
;  APPLICANT: BHAVSAR, SUNIL
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
;  TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
;  FILE REFERENCE: 231/181
;  CURRENT APPLICATION NUMBER: US/09/003,869A
;  CURRENT FILING DATE: 1998-01-07
;  EARLIER APPLICATION NUMBER: US 60/034,905
;  EARLIER FILING DATE: 1997-01-07
;  EARLIER APPLICATION NUMBER: US 60/055,404
;  EARLIER FILING DATE: 1997-08-08
;  EARLIER APPLICATION NUMBER: US 60/065,442
;  EARLIER FILING DATE: 1997-11-14
;  EARLIER APPLICATION NUMBER: US 60/066,029
;  EARLIER FILING DATE: 1997-11-14
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 99
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificially synthesized sequence of novel exendin agonist
```

```
  Query Match             77.7%;  Score 94;  DB 13;  Length 39;
  Best Local Similarity   65.6%;  Pred. No. 3.3e-09;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||| ||||
Db          4 GTFTSDLSKQLEEEAVRLFIEFLKNGGASSGA 35


RESULT 4
US-09-003-869-171
; Sequence 171, Application US/09003869A
; GENERAL INFORMATION:
;  APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
;  APPLICANT: PRICKETT, KATHRYN S.
;  APPLICANT: BHAVSAR, SUNIL
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
;  TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
;  FILE REFERENCE: 231/181
;  CURRENT APPLICATION NUMBER: US/09/003,869A
;  CURRENT FILING DATE: 1998-01-07
;  EARLIER APPLICATION NUMBER: US 60/034,905
;  EARLIER FILING DATE: 1997-01-07
;  EARLIER APPLICATION NUMBER: US 60/055,404
;  EARLIER FILING DATE: 1997-08-08
;  EARLIER APPLICATION NUMBER: US 60/065,442
;  EARLIER FILING DATE: 1997-11-14
;  EARLIER APPLICATION NUMBER: US 60/066,029
;  EARLIER FILING DATE: 1997-11-14
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 171
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificially synthesized sequence of novel exendin agonist
;   OTHER INFORMATION: compound
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (36)...(36)
;   OTHER INFORMATION: amidated Pro (Prolinamide)
US-09-003-869-171

  Query Match             76.9%;  Score 93;  DB 14;  Length 36;
  Best Local Similarity   65.6%;  Pred. No. 4.5e-09;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||| ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 5
US-09-323-867A-171
; Sequence 171, Application US/09323867A
; GENERAL INFORMATION:
;  APPLICANT: Amylin Pharmaceuticals, Inc.
;  APPLICANT:  Young, Andrew et al.
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
;  TITLE OF INVENTION:  OF GESTATIONAL DIABETES MELLITUS
;  FILE REFERENCE: 030639.0032.UTL2 (243/131US)
;  CURRENT APPLICATION NUMBER: US/09/323,867A
;  CURRENT FILING DATE:  1999-06-01
;  NUMBER OF SEQ ID NOS: 189
;  SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 171
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificial sequence with specific variable residues
;   NAME/KEY: MOD_RES
;   LOCATION: (36)
;   OTHER INFORMATION: AMIDATION, Position 36 is Pro-NH2
US-09-323-867A-171

  Query Match             76.9%;  Score 93;  DB 17;  Length 36;
  Best Local Similarity   65.6%;  Pred. No. 4.5e-09;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||| ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 6
US-09-561-226A-166
; Sequence 166, Application US/09561226A
; GENERAL INFORMATION:
;  APPLICANT: Prickett, Kathryn S
;  APPLICANT: Young, Andrew A
;  TITLE OF INVENTION: MODIFIED EXENDINS AND EXENDIN AGONISTS
;  FILE REFERENCE: 030639.0028.UTL(253/204)
;  CURRENT APPLICATION NUMBER: US/09/561,226A
;  CURRENT FILING DATE:  2000-04-28
;  PRIOR APPLICATION NUMBER: 60/132,018
;  PRIOR FILING DATE: 1999-04-30
;  NUMBER OF SEQ ID NOS: 240
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 166
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Amino Acid Sequence
;   NAME/KEY: AMIDATION
;   LOCATION: 36
;   OTHER INFORMATION: Pro in position 36 is amidated
US-09-561-226A-166

  Query Match             76.9%;  Score 93;  DB 19;  Length 36;
  Best Local Similarity   65.6%;  Pred. No. 4.5e-09;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||| ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 7
US-09-561-226D-166
; Sequence 166, Application US/09561226D
; GENERAL INFORMATION:
;  APPLICANT: Prickett, Kathryn S
;  APPLICANT:  Young, Andrew A
;  TITLE OF INVENTION: MODIFIED EXENDINS AND EXENDIN AGONISTS
;  FILE REFERENCE: 030639.0028.UTL(253/204)
;  CURRENT APPLICATION NUMBER: US/09/561,226D
;  CURRENT FILING DATE:  2000-04-28
;  PRIOR APPLICATION NUMBER: 60/132,018
;  PRIOR FILING DATE: 1999-04-30
;  NUMBER OF SEQ ID NOS: 240
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 166
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Amino Acid Sequence
;   NAME/KEY: AMIDATION
;   LOCATION: 36
;   OTHER INFORMATION: Pro in position 36 is amidated
US-09-561-226D-166

  Query Match             76.9%;  Score 93;  DB 19;  Length 36;
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;       FILING DATE:  08-AUGUST-1996
;       CLASSIFICATION:  514
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  DUFT, BRADFORD J.
;       REGISTRATION NUMBER:  32,219
;       REFERENCE/DOCKET NUMBER:  227/166
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  619/552-2200
;       TELEFAX:  213/955-0440
;       TELEX:  67-3510
;   INFORMATION FOR SEQ ID NO:  35:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  39 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FEATURE:
;       LOCATION:  31, 36, 37, 38
;       OTHER INFORMATION:  N-methylalanine
;       LOCATION:  39
;       OTHER INFORMATION:  amidated Ser (Serineamide)
US-08-908-867-35

  Query Match             77.7%;  Score 94;  DB 13;  Length 39;
  Best Local Similarity   65.6%;  Pred. No. 3.3e-09;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||| ||||
Db          4 GTFTSDLSKQLEEEAVRLFIEFLKNGGASSGA 35


RESULT 2
US-08-908-867A-35
; Sequence 35, Application US/08908867A
;  GENERAL INFORMATION:
;     APPLICANT:  YOUNG, Andrew A.
;     APPLICANT:  GEDULIN, Bronislava
;     APPLICANT:  BEELEY, Nigel Robert Arnold
;     APPLICANT:  PRICKETT, Kathryn S.
;     TITLE OF INVENTION:  METHODS FOR REGULATING
;     TITLE OF INVENTION:  GASTROINTESTINAL MOTILITY
;     NUMBER OF SEQUENCES:  37
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  LYON & LYON
;       STREET:  633 WEST FIFTH STREET
;       CITY:  LOS ANGELES
;       STATE:  CALIFORNIA
;       COUNTRY:  USA
;       ZIP:  90017
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/908,867A
;       FILING DATE:  08-AUGUST-1997
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/694,954
;       FILING DATE:  08-AUGUST-1996
;       CLASSIFICATION:  514
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  DUFT, BRADFORD J.
;       REGISTRATION NUMBER:  32,219
;       REFERENCE/DOCKET NUMBER:  227/166
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  619/552-2200
;       TELEFAX:  213/955-0440
;       TELEX:  67-3510
;   INFORMATION FOR SEQ ID NO:  35:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  39 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FEATURE:
;       LOCATION:  31, 36, 37, 38
;       OTHER INFORMATION:  N-methylalanine
;       LOCATION:  39
;       OTHER INFORMATION:  amidated Ser (Serineamide)
US-08-908-867A-35

  Query Match             77.7%;  Score 94;  DB 13;  Length 39;
  Best Local Similarity   65.6%;  Pred. No. 3.3e-09;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||| ||||
Db          4 GTFTSDLSKQLEEEAVRLFIEFLKNGGASSGA 35


RESULT 3
US-08-908-867-35
; Sequence 35, Application US/08908867B
;  GENERAL INFORMATION:
;       APPLICANT: YOUNG, ANDREW A.
;                  GEDULIN, BRONISLAVA
;                  BEELEY, NIGEL ROBERT ARNOLD
;                  PRICKETT, KATHRYN S.
;       TITLE OF INVENTION: METHODS FOR REGULATING
;                           GASTROINTESTINAL MOTIITY
;       NUMBER OF SEQUENCES: 39
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: LYON & LYON
;            STREET: 633 WEST FIFTH STREET
;            CITY: LOS ANGELES
;            STATE: CALIFORNIA
;            COUNTRY: USA
;            ZIP: 90017
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/908,867B
;            FILING DATE: 08-Aug-1997
;            CLASSIFICATION: Pending
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/694,954
;            FILING DATE: 08-AUGUST-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BERKMAN, CHARLES S.
;            REGISTRATION NUMBER: 38,077
;            REFERENCE/DOCKET NUMBER: 227/166
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 619/552-2200
;            TELEFAX: 213/955-0440
;            TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 35
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 39 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       FEATURE:
;            LOCATION:  39
;            OTHER INFORMATION:  amidated Ser (Serineamide)
;       SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-08-908-867-35
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OM protein - protein search, using sw model

Run on: June 24, 2003, 23:05:25 ; Search time 221 Seconds
(without alignments)
116.694 Million cell updates/sec

Title: US-09-889-331A-47
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Searched: 4569144 seqs, 644733110 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/paa/US082_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*
8: /cgn2_6/ptodata/1/paa/US084_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	94	77.7	39	13	US-08-908-867-35	Sequence 35, Appl
2	94	77.7	39	13	US-08-908-867A-35	Sequence 35, Appl
3	94	77.7	39	13	US-08-908-867-35	Sequence 35, Appl
4	93	76.9	36	14	US-09-003-869-171	Sequence 171, App
5	93	76.9	36	17	US-09-323-867A-171	Sequence 171, App
6	93	76.9	36	19	US-09-561-226A-166	Sequence 166, App
7	93	76.9	36	19	US-09-561-226D-166	Sequence 166, App
8	93	76.9	36	21	US-09-756-690A-171	Sequence 171, App
9	93	76.9	36	22	US-09-889-331-189	Sequence 189, App
10	93	76.9	36	23	US-09-554-531A-76	Sequence 76, Appl
11	93	76.9	37	14	US-09-003-869-99	Sequence 99, Appl
12	93	76.9	37	14	US-09-003-869-183	Sequence 183, App
13	93	76.9	37	17	US-09-323-867A-99	Sequence 99, Appl
14	93	76.9	37	17	US-09-323-867A-183	Sequence 183, App
15	93	76.9	37	19	US-09-561-226A-86	Sequence 86, Appl
16	93	76.9	37	19	US-09-561-226A-178	Sequence 178, App
17	93	76.9	37	19	US-09-561-226D-86	Sequence 86, Appl
18	93	76.9	37	19	US-09-561-226D-178	Sequence 178, App
19	93	76.9	37	20	US-09-622-105-65	Sequence 65, Appl
20	93	76.9	37	21	US-09-756-690A-99	Sequence 99, Appl
21	93	76.9	37	21	US-09-756-690A-183	Sequence 183, App
22	93	76.9	37	22	US-09-889-331-109	Sequence 109, App
23	93	76.9	37	22	US-09-889-331-201	Sequence 201, App
24	93	76.9	37	23	US-09-554-531A-88	Sequence 88, Appl
25	93	76.9	39	13	US-08-908-867-33	Sequence 33, Appl
26	93	76.9	39	13	US-08-908-867A-33	Sequence 33, Appl
27	93	76.9	39	13	US-08-908-867-33	Sequence 33, Appl
28	93	76.9	39	14	US-09-003-869-35	Sequence 35, Appl
29	93	76.9	39	14	US-09-003-869-36	Sequence 36, Appl
30	93	76.9	39	14	US-09-003-869-39	Sequence 39, Appl
31	93	76.9	39	17	US-09-323-867A-35	Sequence 35, Appl
32	93	76.9	39	17	US-09-323-867A-36	Sequence 36, Appl
33	93	76.9	39	17	US-09-323-867A-39	Sequence 39, Appl
34	93	76.9	39	19	US-09-561-226-36	Sequence 36, Appl
35	93	76.9	39	19	US-09-561-226-37	Sequence 37, Appl
36	93	76.9	39	19	US-09-561-226-40	Sequence 40, Appl
37	93	76.9	39	21	US-09-756-690A-35	Sequence 35, Appl
38	93	76.9	39	21	US-09-756-690A-36	Sequence 36, Appl
39	93	76.9	39	21	US-09-756-690A-39	Sequence 39, Appl
40	93	76.9	39	22	US-09-889-331-36	Sequence 36, Appl
41	93	76.9	39	22	US-09-889-331-37	Sequence 37, Appl
42	93	76.9	39	22	US-09-889-331-40	Sequence 40, Appl
43	92	76.0	35	14	US-09-003-869-69	Sequence 69, Appl
44	92	76.0	35	14	US-09-003-869-173	Sequence 173, App
45	92	76.0	35	17	US-09-323-867A-69	Sequence 69, Appl

ALIGNMENTS

RESULT 1
US-08-908-867-35
; Sequence 35, Application US/08908867
; GENERAL INFORMATION:
; APPLICANT: YOUNG, Andrew A.
; APPLICANT: GEDULIN, Bronislava
; APPLICANT: BEELEY, Nigel Robert Arnold
; APPLICANT: PRICKETT, Kathryn S.
; TITLE OF INVENTION: METHODS FOR REGULATING
; TITLE OF INVENTION: GASTROINTESTINAL MOTIITY
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LYON & LYON
; STREET: 633 WEST FIFTH STREET
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,867
; FILING DATE: 08-AUGUST-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/694,954

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RESULT 15
US-10-342-014-183
; Sequence 183, Application US/10342014
; GENERAL INFORMATION:
;  APPLICANT: Amylin Pharmaceuticals, Inc.
;  APPLICANT:  Hiles, Richard A. et al.
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
;  TITLE OF INVENTION:  OF GESTATIONAL DIABETES MELLITUS
;  FILE REFERENCE: 18528.169 (0204-CON-0)
;  CURRENT APPLICATION NUMBER: US/10/342,014
;  CURRENT FILING DATE:  2003-01-13
;  PRIOR APPLICATION NUMBER: 09/323,867
;  PRIOR FILING DATE: 1999-06-01
;  NUMBER OF SEQ ID NOS: 189
;  SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 183
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificial sequence with specific variable residues
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (31)
;   OTHER INFORMATION: Xaa is N-methylalanine
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (36)..(37)
;   OTHER INFORMATION: Xaa is N-methylalanine
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (37)
;   OTHER INFORMATION: AMIDATION, Position 37 is N-methylalanine-NH2
US-10-342-014-183

  Query Match             76.9%;  Score 93;  DB 6;  Length 37;
  Best Local Similarity   68.8%;  Pred. No. 7.8e-10;
  Matches   22;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||||||||
Db          4 GTFTSALSKQMEEEAVRLFIEWLKNGGXSSGA 35


Search completed: June 24, 2003, 23:19:19
Job time : 73.5 secs
```

```
  Matches   22;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||||||||
Db          4 GTFTSALSKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 12
US-10-157-224A-99
; Sequence 99, Application US/10157224A
; GENERAL INFORMATION:
;  APPLICANT: YOUNG, ANDREW A.
;  APPLICANT:  KOLTERMAN, ORVILLE G.
;  TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
;  TITLE OF INVENTION:  ADMINISTRATION THEREOF
;  FILE REFERENCE: 02001-050
;  CURRENT APPLICATION NUMBER: US/10/157,224A
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: 09/889,330
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: PCT/US00/00902
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 60/116,380
;  PRIOR FILING DATE: 1999-01-14
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
;   FEATURE:
;   OTHER INFORMATION: c-term amidation
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (31)
;   OTHER INFORMATION: Homoproline
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (36)..(37)
;   OTHER INFORMATION: Homoproline
US-10-157-224A-99

  Query Match            76.9%;  Score 93;  DB 6;  Length 37;
  Best Local Similarity   68.8%;  Pred. No. 7.8e-10;
  Matches   22;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||||||||
Db          4 GTFTSDASKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 13
US-10-157-224A-183
; Sequence 183, Application US/10157224A
; GENERAL INFORMATION:
;  APPLICANT: YOUNG, ANDREW A.
;  APPLICANT:  KOLTERMAN, ORVILLE G.
;  TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
;  TITLE OF INVENTION:  ADMINISTRATION THEREOF
;  FILE REFERENCE: 02001-050
;  CURRENT APPLICATION NUMBER: US/10/157,224A
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: 09/889,330
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: PCT/US00/00902
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 60/116,380
;  PRIOR FILING DATE: 1999-01-14
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 183
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
;   FEATURE:
;   OTHER INFORMATION: c-term amidation
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (31)
;   OTHER INFORMATION: N-methylalanine
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (36)..(37)
;   OTHER INFORMATION: N-methylalanine
US-10-157-224A-183

  Query Match            76.9%;  Score 93;  DB 6;  Length 37;
  Best Local Similarity   68.8%;  Pred. No. 7.8e-10;
  Matches   22;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||||||||
Db          4 GTFTSALSKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 14
US-10-342-014-99
; Sequence 99, Application US/10342014
; GENERAL INFORMATION:
;  APPLICANT: Amylin Pharmaceuticals, Inc.
;  APPLICANT:  Hiles, Richard A. et al.
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
;  TITLE OF INVENTION:  OF GESTATIONAL DIABETES MELLITUS
;  FILE REFERENCE: 18528.169 (0204-CON-0)
;  CURRENT APPLICATION NUMBER: US/10/342,014
;  CURRENT FILING DATE:  2003-01-13
;  PRIOR APPLICATION NUMBER: 09/323,867
;  PRIOR FILING DATE: 1999-06-01
;  NUMBER OF SEQ ID NOS: 189
;  SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 99
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificial sequence with specific variable residues
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (31)
;   OTHER INFORMATION: Xaa is homoproline
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (36)..(37)
;   OTHER INFORMATION: Xaa is homoproline
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (37)
;   OTHER INFORMATION: AMIDATION, Position 37 is homoproline-NH2
US-10-342-014-99

  Query Match            76.9%;  Score 93;  DB 6;  Length 37;
  Best Local Similarity   68.8%;  Pred. No. 7.8e-10;
  Matches   22;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||||||||
Db          4 GTFTSDASKQMEEEAVRLFIEWLKNGGXSSGA 35
```

```
Db          4 GTFTSDASKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 9
US-09-889-331A-201
; Sequence 201, Application US/09889331A
; GENERAL INFORMATION:
;  APPLICANT: YOUNG, ANDREW A.
;  APPLICANT:  GEDULIN, BRONISLAVA
;  TITLE OF INVENTION: METHODS FOR GLUCAGON SUPPRESSION
;  FILE REFERENCE: 030639.0031.UTL1 (249/167)
;  CURRENT APPLICATION NUMBER: US/09/889,331A
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: PCT/US00/00942
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 60/116,380
;  PRIOR FILING DATE: 1999-01-14
;  PRIOR APPLICATION NUMBER: 60/132,017
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 239
;  SOFTWARE: FastSEQ for Windows Version 4.0
;    Microsoft WORD 97 SR-2
; SEQ ID NO 201
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Amino Acid Sequence
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (31)
;   OTHER INFORMATION: Xaa in position 31 stands for Nme
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (36)..(37)
;   OTHER INFORMATION: Xaa in positions 36-37 stands for Nme
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (37)
;   OTHER INFORMATION: Nme in position 37 is amidated
US-09-889-331A-201

  Query Match             76.9%;  Score 93;  DB 5;  Length 37;
  Best Local Similarity   68.8%;  Pred. No. 7.8e-10;
  Matches   22;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||||||||
Db          4 GTFTSALSKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 10
US-10-187-051-99
; Sequence 99, Application US/10187051
; GENERAL INFORMATION:
;  APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
;  APPLICANT:  PRICKETT, KATHRYN S.
;  APPLICANT:  BHAVSAR, SUNIL
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
;  TITLE OF INVENTION:  THE REDUCTION OF FOOD INTAKE
;  FILE REFERENCE: 231/181
;  CURRENT APPLICATION NUMBER: US/10/187,051
;  CURRENT FILING DATE:  2002-06-28
;  PRIOR APPLICATION NUMBER: US/09/003,869
;  PRIOR FILING DATE: 1998-01-07
;  PRIOR APPLICATION NUMBER: US 60/034,905
;  PRIOR FILING DATE: 1997-01-07
;  PRIOR APPLICATION NUMBER: US 60/055,404
;  PRIOR FILING DATE: 1997-08-08
;  PRIOR APPLICATION NUMBER: US 60/065,442
;  PRIOR FILING DATE: 1997-11-14
;  PRIOR APPLICATION NUMBER: US 60/066,029
;  PRIOR FILING DATE: 1997-11-14
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 99
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificially synthesized sequence of novel exendin
;   OTHER INFORMATION: agonist
;   OTHER INFORMATION: compound
;   FEATURE:
;   OTHER INFORMATION: Xaa in positions 31, 36 and 37 stands for homoproline.
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (37)...(37)
;   OTHER INFORMATION: amidated hPro (homoprolinamide)
US-10-187-051-99

  Query Match             76.9%;  Score 93;  DB 6;  Length 37;
  Best Local Similarity   68.8%;  Pred. No. 7.8e-10;
  Matches   22;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||||||||
Db          4 GTFTSDASKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 11
US-10-187-051-183
; Sequence 183, Application US/10187051
; GENERAL INFORMATION:
;  APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
;  APPLICANT:  PRICKETT, KATHRYN S.
;  APPLICANT:  BHAVSAR, SUNIL
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
;  TITLE OF INVENTION:  THE REDUCTION OF FOOD INTAKE
;  FILE REFERENCE: 231/181
;  CURRENT APPLICATION NUMBER: US/10/187,051
;  CURRENT FILING DATE:  2002-06-28
;  PRIOR APPLICATION NUMBER: US/09/003,869
;  PRIOR FILING DATE: 1998-01-07
;  PRIOR APPLICATION NUMBER: US 60/034,905
;  PRIOR FILING DATE: 1997-01-07
;  PRIOR APPLICATION NUMBER: US 60/055,404
;  PRIOR FILING DATE: 1997-08-08
;  PRIOR APPLICATION NUMBER: US 60/065,442
;  PRIOR FILING DATE: 1997-11-14
;  PRIOR APPLICATION NUMBER: US 60/066,029
;  PRIOR FILING DATE: 1997-11-14
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 183
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificially synthesized sequence of novel exendin
;   OTHER INFORMATION: agonist
;   OTHER INFORMATION: compound
;   FEATURE:
;   OTHER INFORMATION: Xaa in positions 31, 36 and 37 stands for n-
;   OTHER INFORMATION: methylalanine.
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (37)...(37)
;   OTHER INFORMATION: amidated Nmeala (n-methylalaninamide)
US-10-187-051-183

  Query Match             76.9%;  Score 93;  DB 6;  Length 37;
  Best Local Similarity   68.8%;  Pred. No. 7.8e-10;
```

```
  Best Local Similarity   65.6%;  Pred. No. 7.6e-10;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||| ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 6
PCT-US03-16699-99
; Sequence 99, Application PC/TUS0316699
; GENERAL INFORMATION:
;  APPLICANT: Amylin Pharmaceuticals, Inc.
;  APPLICANT:  Young, Andrew A. et al.
;  TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF ADMINISTRATIO T
;  FILE REFERENCE: 18528.464 (0201-CIP-5)
;  CURRENT APPLICATION NUMBER: PCT/US03/16699
;  CURRENT FILING DATE:  2003-05-28
;  PRIOR APPLICATION NUMBER: 10/157,224
;  PRIOR FILING DATE: 2002-05-28
;  PRIOR APPLICATION NUMBER: <NOT YET ASSIGNED>
;  PRIOR FILING DATE: 2002-05-28
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 99
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificial sequence with specific variable residues
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (31)
;   OTHER INFORMATION: Xaa is homoproline
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (36)..(37)
;   OTHER INFORMATION: Xaa is homoproline
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (37)
;   OTHER INFORMATION: AMIDATION, Position 37 is homoproline-NH2
PCT-US03-16699-99

  Query Match             76.9%;  Score 93;  DB 1;  Length 37;
  Best Local Similarity   68.8%;  Pred. No. 7.8e-10;
  Matches   22;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||||||||
Db          4 GTFTSDASKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 7
PCT-US03-16699-183
; Sequence 183, Application PC/TUS0316699
; GENERAL INFORMATION:
;  APPLICANT: Amylin Pharmaceuticals, Inc.
;  APPLICANT:  Young, Andrew A. et al.
;  TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF ADMINISTRATIO T
;  FILE REFERENCE: 18528.464 (0201-CIP-5)
;  CURRENT APPLICATION NUMBER: PCT/US03/16699
;  CURRENT FILING DATE:  2003-05-28
;  PRIOR APPLICATION NUMBER: 10/157,224
;  PRIOR FILING DATE: 2002-05-28
;  PRIOR APPLICATION NUMBER: <NOT YET ASSIGNED>
;  PRIOR FILING DATE: 2002-05-28
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 183
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificial sequence with specific variable residues
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (31)
;   OTHER INFORMATION: Xaa is N-methylalanine
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (36)..(37)
;   OTHER INFORMATION: Xaa is N-methylalanine
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (37)
;   OTHER INFORMATION: AMIDATION, Position 37 is N-methylalanine-NH2
PCT-US03-16699-183

  Query Match             76.9%;  Score 93;  DB 1;  Length 37;
  Best Local Similarity   68.8%;  Pred. No. 7.8e-10;
  Matches   22;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||||||||
Db          4 GTFTSALSKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 8
US-09-889-331A-109
; Sequence 109, Application US/09889331A
; GENERAL INFORMATION:
;  APPLICANT: YOUNG, ANDREW A.
;  APPLICANT:  GEDULIN, BRONISLAVA
;  TITLE OF INVENTION: METHODS FOR GLUCAGON SUPPRESSION
;  FILE REFERENCE: 030639.0031.UTL1 (249/167)
;  CURRENT APPLICATION NUMBER: US/09/889,331A
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: PCT/US00/00942
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 60/116,380
;  PRIOR FILING DATE: 1999-01-14
;  PRIOR APPLICATION NUMBER: 60/132,017
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 239
;  SOFTWARE: FastSEQ for Windows Version 4.0
;    Microsoft WORD 97 SR-2
; SEQ ID NO 109
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Amino Acid Sequence
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (31)
;   OTHER INFORMATION: Xaa in position 31 stands for hPro
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (36)..(37)
;   OTHER INFORMATION: Xaa in positions 36-37 stands for hPro
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (37)
;   OTHER INFORMATION: hPro in position 37 is amidated
US-09-889-331A-109

  Query Match             76.9%;  Score 93;  DB 5;  Length 37;
  Best Local Similarity   68.8%;  Pred. No. 7.8e-10;
  Matches   22;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||||||||
```

```
;  PRIOR APPLICATION NUMBER: 60/116,380
;  PRIOR FILING DATE: 1999-01-14
;  PRIOR APPLICATION NUMBER: 60/132,017
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 239
;  SOFTWARE: FastSEQ for Windows Version 4.0
;    Microsoft WORD 97 SR-2
; SEQ ID NO 189
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Amino Acid Sequence
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (36)
;   OTHER INFORMATION: Pro in position 36 is amidated
US-09-889-331A-189

  Query Match             76.9%;  Score 93;  DB 5;  Length 36;
  Best Local Similarity   65.6%;  Pred. No. 7.6e-10;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||| ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 3
US-10-187-051-171
; Sequence 171, Application US/10187051
; GENERAL INFORMATION:
;  APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
;  APPLICANT:  PRICKETT, KATHRYN S.
;  APPLICANT:  BHAVSAR, SUNIL
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
;  TITLE OF INVENTION:  THE REDUCTION OF FOOD INTAKE
;  FILE REFERENCE: 231/181
;  CURRENT APPLICATION NUMBER: US/10/187,051
;  CURRENT FILING DATE:  2002-06-28
;  PRIOR APPLICATION NUMBER: US/09/003,869
;  PRIOR FILING DATE: 1998-01-07
;  PRIOR APPLICATION NUMBER: US 60/034,905
;  PRIOR FILING DATE: 1997-01-07
;  PRIOR APPLICATION NUMBER: US 60/055,404
;  PRIOR FILING DATE: 1997-08-08
;  PRIOR APPLICATION NUMBER: US 60/065,442
;  PRIOR FILING DATE: 1997-11-14
;  PRIOR APPLICATION NUMBER: US 60/066,029
;  PRIOR FILING DATE: 1997-11-14
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 171
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificially synthesized sequence of novel exendin
;   OTHER INFORMATION: agonist
;   OTHER INFORMATION: compound
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (36)...(36)
;   OTHER INFORMATION: amidated Pro (Prolinamide)
US-10-187-051-171

  Query Match             76.9%;  Score 93;  DB 6;  Length 36;
  Best Local Similarity   65.6%;  Pred. No. 7.6e-10;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||| ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 4
US-10-157-224A-171
; Sequence 171, Application US/10157224A
; GENERAL INFORMATION:
;  APPLICANT: YOUNG, ANDREW A.
;  APPLICANT:  KOLTERMAN, ORVILLE G.
;  TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
;  TITLE OF INVENTION:  ADMINISTRATION THEREOF
;  FILE REFERENCE: 02001-050
;  CURRENT APPLICATION NUMBER: US/10/157,224A
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: 09/889,330
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: PCT/US00/00902
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 60/116,380
;  PRIOR FILING DATE: 1999-01-14
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 171
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
;   FEATURE:
;   OTHER INFORMATION: c-term amidation
US-10-157-224A-171

  Query Match             76.9%;  Score 93;  DB 6;  Length 36;
  Best Local Similarity   65.6%;  Pred. No. 7.6e-10;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||| ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 5
US-10-342-014-171
; Sequence 171, Application US/10342014
; GENERAL INFORMATION:
;  APPLICANT: Amylin Pharmaceuticals, Inc.
;  APPLICANT:  Hiles, Richard A. et al.
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
;  TITLE OF INVENTION:  OF GESTATIONAL DIABETES MELLITUS
;  FILE REFERENCE: 18528.169 (0204-CON-0)
;  CURRENT APPLICATION NUMBER: US/10/342,014
;  CURRENT FILING DATE:  2003-01-13
;  PRIOR APPLICATION NUMBER: 09/323,867
;  PRIOR FILING DATE: 1999-06-01
;  NUMBER OF SEQ ID NOS: 189
;  SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 171
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificial sequence with specific variable residues
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (36)
;   OTHER INFORMATION: AMIDATION, Position 36 is Pro-NH2
US-10-342-014-171

  Query Match             76.9%;  Score 93;  DB 6;  Length 36;
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 24, 2003, 23:06:00 ; Search time 72.5 Seconds
(without alignments)
141.898 Million cell updates/sec

Title: US-09-889-331A-47
Perfect score: 121
Sequence: 1 XXXGTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGAXXXXX 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1171708 seqs, 257189365 residues

Total number of hits satisfying chosen parameters: 1171708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	93	76.9	36	1	PCT-US03-16699-171	Sequence 171, App
2	93	76.9	36	5	US-09-889-331A-189	Sequence 189, App
3	93	76.9	36	6	US-10-187-051-171	Sequence 171, App
4	93	76.9	36	6	US-10-157-224A-171	Sequence 171, App
5	93	76.9	36	6	US-10-342-014-171	Sequence 171, App
6	93	76.9	37	1	PCT-US03-16699-99	Sequence 99, Appl
7	93	76.9	37	1	PCT-US03-16699-183	Sequence 183, App
8	93	76.9	37	5	US-09-889-331A-109	Sequence 109, App
9	93	76.9	37	5	US-09-889-331A-201	Sequence 201, App
10	93	76.9	37	6	US-10-187-051-99	Sequence 99, Appl
11	93	76.9	37	6	US-10-187-051-183	Sequence 183, App
12	93	76.9	37	6	US-10-157-224A-99	Sequence 99, Appl
13	93	76.9	37	6	US-10-157-224A-183	Sequence 183, App
14	93	76.9	37	6	US-10-342-014-99	Sequence 99, Appl
15	93	76.9	37	6	US-10-342-014-183	Sequence 183, App
16	93	76.9	39	1	PCT-US03-16699-35	Sequence 35, Appl
17	93	76.9	39	1	PCT-US03-16699-36	Sequence 36, Appl
18	93	76.9	39	1	PCT-US03-16699-39	Sequence 39, Appl
19	93	76.9	39	5	US-09-889-331A-36	Sequence 36, Appl
20	93	76.9	39	5	US-09-889-331A-37	Sequence 37, Appl
21	93	76.9	39	5	US-09-889-331A-40	Sequence 40, Appl
22	93	76.9	39	6	US-10-187-051-35	Sequence 35, Appl
23	93	76.9	39	6	US-10-187-051-36	Sequence 36, Appl
24	93	76.9	39	6	US-10-187-051-39	Sequence 39, Appl
25	93	76.9	39	6	US-10-157-224A-35	Sequence 35, Appl
26	93	76.9	39	6	US-10-157-224A-36	Sequence 36, Appl
27	93	76.9	39	6	US-10-157-224A-39	Sequence 39, Appl
28	93	76.9	39	6	US-10-342-014-35	Sequence 35, Appl
29	93	76.9	39	6	US-10-342-014-36	Sequence 36, Appl
30	93	76.9	39	6	US-10-342-014-39	Sequence 39, Appl
31	92	76.0	35	1	PCT-US03-16699-69	Sequence 69, Appl
32	92	76.0	35	1	PCT-US03-16699-173	Sequence 173, App
33	92	76.0	35	5	US-09-889-331A-79	Sequence 79, Appl
34	92	76.0	35	5	US-09-889-331A-191	Sequence 191, App
35	92	76.0	35	6	US-10-187-051-69	Sequence 69, Appl
36	92	76.0	35	6	US-10-187-051-173	Sequence 173, App
37	92	76.0	35	6	US-10-157-224A-69	Sequence 69, Appl
38	92	76.0	35	6	US-10-157-224A-173	Sequence 173, App
39	92	76.0	35	6	US-10-342-014-69	Sequence 69, Appl
40	92	76.0	35	6	US-10-342-014-173	Sequence 173, App
41	92	76.0	36	1	PCT-US03-16699-67	Sequence 67, Appl
42	92	76.0	36	1	PCT-US03-16699-86	Sequence 86, Appl
43	92	76.0	36	1	PCT-US03-16699-170	Sequence 170, App
44	92	76.0	36	1	PCT-US03-16699-184	Sequence 184, App
45	92	76.0	36	5	US-09-889-331A-77	Sequence 77, Appl

ALIGNMENTS

RESULT 1
PCT-US03-16699-171
; Sequence 171, Application PC/TUS0316699
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Young, Andrew A. et al.
; TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF ADMINISTRATI
; FILE REFERENCE: 18528.464 (0201-CIP-5)
; CURRENT APPLICATION NUMBER: PCT/US03/16699
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 10/157,224
; PRIOR FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: <NOT YET ASSIGNED>
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 188
; SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 171
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence with specific variable residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (36)
; OTHER INFORMATION: AMIDATION, Position 36 is Pro-NH2
PCT-US03-16699-171

Query Match 76.9%; Score 93; DB 1; Length 36;
Best Local Similarity 65.6%; Pred. No. 7.6e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

```
Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| ||||||| |||| |||| .
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35
```

RESULT 2
US-09-889-331A-189
; Sequence 189, Application US/09889331A
; GENERAL INFORMATION:
; APPLICANT: YOUNG, ANDREW A.
; APPLICANT: GEDULIN, BRONISLAVA
; TITLE OF INVENTION: METHODS FOR GLUCAGON SUPPRESSION
; FILE REFERENCE: 030639.0031.UTL1 (249/167)
; CURRENT APPLICATION NUMBER: US/09/889,331A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/00942
; PRIOR FILING DATE: 2000-01-14

```
RESULT 14
US-09-554-531A-76
; Sequence 76, Application US/09554531A
; GENERAL INFORMATION:
;  APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
;  APPLICANT:  PRICKETT, KATHRYN S.
;  TITLE OF INVENTION: NOVEL EXENDIN AGONIST COMPOUNDS
;  FILE REFERENCE: 238/087 US
;  CURRENT APPLICATION NUMBER: US/09/554,531A
;  CURRENT FILING DATE:  2000-08-08
;  PRIOR APPLICATION NUMBER: PCT/US98/24273
;  PRIOR FILING DATE: 1998-11-13
;  PRIOR APPLICATION NUMBER: 60/066,029
;  PRIOR FILING DATE: 1997-11-14
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exendin agonist
;   FEATURE:
;   OTHER INFORMATION: c-term amidation
US-09-554-531A-76

  Query Match             62.9%;  Score 70.5;  DB 23;  Length 36;
  Best Local Similarity   59.4%;  Pred. No. 1.8e-05;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 15
US-09-003-869-99
; Sequence 99, Application US/09003869A
; GENERAL INFORMATION:
;  APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
;  APPLICANT: PRICKETT, KATHRYN S.
;  APPLICANT: BHAVSAR, SUNIL
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
;  TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
;  FILE REFERENCE: 231/181
;  CURRENT APPLICATION NUMBER: US/09/003,869A
;  CURRENT FILING DATE: 1998-01-07
;  EARLIER APPLICATION NUMBER: US 60/034,905
;  EARLIER FILING DATE: 1997-01-07
;  EARLIER APPLICATION NUMBER: US 60/055,404
;  EARLIER FILING DATE: 1997-08-08
;  EARLIER APPLICATION NUMBER: US 60/065,442
;  EARLIER FILING DATE: 1997-11-14
;  EARLIER APPLICATION NUMBER: US 60/066,029
;  EARLIER FILING DATE: 1997-11-14
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 99
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificially synthesized sequence of novel exendin agonist
;   OTHER INFORMATION: compound
;   FEATURE:
;   OTHER INFORMATION: Xaa in positions 31, 36 and 37 stands for homoproline.
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (37)...(37)
;   OTHER INFORMATION: amidated hPro (homoprolinamide)
US-09-003-869-99

  Query Match             62.9%;  Score 70.5;  DB 14;  Length 37;
  Best Local Similarity   62.5%;  Pred. No. 1.8e-05;
  Matches   20;  Conservative    0;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  |||||||
Db          4 GTFTSDASKQMEEEAVRLFIEWLKNGGXSSGA 35


Search completed: June 24, 2003, 23:16:46
Job time : 221 secs
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Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 10
US-09-561-226A-166
; Sequence 166, Application US/09561226A
; GENERAL INFORMATION:
;  APPLICANT: Prickett, Kathryn S
;  APPLICANT:  Young, Andrew A
;  TITLE OF INVENTION: MODIFIED EXENDINS AND EXENDIN AGONISTS
;  FILE REFERENCE: 030639.0028.UTL(253/204)
;  CURRENT APPLICATION NUMBER: US/09/561,226A
;  CURRENT FILING DATE:  2000-04-28
;  PRIOR APPLICATION NUMBER: 60/132,018
;  PRIOR FILING DATE: 1999-04-30
;  NUMBER OF SEQ ID NOS: 240
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 166
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Amino Acid Sequence
;   NAME/KEY: AMIDATION
;   LOCATION: 36
;   OTHER INFORMATION: Pro in position 36 is amidated
US-09-561-226A-166

  Query Match             62.9%;  Score 70.5;  DB 19;  Length 36;
  Best Local Similarity   59.4%;  Pred. No. 1.8e-05;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 11
US-09-561-226D-166
; Sequence 166, Application US/09561226D
; GENERAL INFORMATION:
;  APPLICANT: Prickett, Kathryn S
;  APPLICANT:  Young, Andrew A
;  TITLE OF INVENTION: MODIFIED EXENDINS AND EXENDIN AGONISTS
;  FILE REFERENCE: 030639.0028.UTL(253/204)
;  CURRENT APPLICATION NUMBER: US/09/561,226D
;  CURRENT FILING DATE:  2000-04-28
;  PRIOR APPLICATION NUMBER: 60/132,018
;  PRIOR FILING DATE: 1999-04-30
;  NUMBER OF SEQ ID NOS: 240
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 166
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Amino Acid Sequence
;   NAME/KEY: AMIDATION
;   LOCATION: 36
;   OTHER INFORMATION: Pro in position 36 is amidated
US-09-561-226D-166

  Query Match             62.9%;  Score 70.5;  DB 19;  Length 36;
  Best Local Similarity   59.4%;  Pred. No. 1.8e-05;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 12
US-09-756-690A-171
; Sequence 171, Application US/09756690A
; GENERAL INFORMATION:
;  APPLICANT: KOLTERMAN, ORVILLE G.
;  APPLICANT:  YOUNG, ANDREW A.
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF
;  TITLE OF INVENTION:  TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
;  FILE REFERENCE: 249/124
;  CURRENT APPLICATION NUMBER: US/09/756,690A
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: PatentIn Ver 2.1
; SEQ ID NO 171
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
;   FEATURE:
;   OTHER INFORMATION: c-term amidation
US-09-756-690A-171

  Query Match             62.9%;  Score 70.5;  DB 21;  Length 36;
  Best Local Similarity   59.4%;  Pred. No. 1.8e-05;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 13
US-09-889-331-189
; Sequence 189, Application US/09889331
; GENERAL INFORMATION:
;  APPLICANT: YOUNG, ANDREW A.
;  APPLICANT:  GEDULIN, BRONISLAVA
;  TITLE OF INVENTION: METHODS FOR GLUCAGON SUPPRESSION
;  FILE REFERENCE: 030639.0031.UTL1 (249/167)
;  CURRENT APPLICATION NUMBER: US/09/889,331
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: PCT/US00/00942
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 60/116,380
;  PRIOR FILING DATE: 1999-01-14
;  PRIOR APPLICATION NUMBER: 60/132,017
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 239
;  SOFTWARE: FastSEQ for Windows Version 4.0, Microsoft WORD 97 SR-2
; SEQ ID NO 189
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Amino Acid Sequence
;   NAME/KEY: AMIDATION
;   LOCATION: (36)
;   OTHER INFORMATION: Pro in position 36 is amidated
US-09-889-331-189

  Query Match             62.9%;  Score 70.5;  DB 22;  Length 36;
  Best Local Similarity   59.4%;  Pred. No. 1.8e-05;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35
```

```
;      OTHER INFORMATION:  amidated Ser (Serineamide)
US-08-908-867A-35

  Query Match             63.8%;  Score 71.5;  DB 13;  Length 39;
  Best Local Similarity   59.4%;  Pred. No. 1.3e-05;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDLSKQLEEEAVRLFIEFLKNGGASSGA 35


RESULT 7
US-08-908-867-35
; Sequence 35, Application US/08908867B
;   GENERAL INFORMATION:
;        APPLICANT: YOUNG, ANDREW A.
;                   GEDULIN, BRONISLAVA
;                   BEELEY, NIGEL ROBERT ARNOLD
;                   PRICKETT, KATHRYN S.
;        TITLE OF INVENTION: METHODS FOR REGULATING
;                            GASTROINTESTINAL MOTIITY
;        NUMBER OF SEQUENCES: 39
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: LYON & LYON
;             STREET: 633 WEST FIFTH STREET
;             CITY: LOS ANGELES
;             STATE: CALIFORNIA
;             COUNTRY: USA
;             ZIP: 90017
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/908,867B
;             FILING DATE: 08-Aug-1997
;             CLASSIFICATION: Pending
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/694,954
;             FILING DATE: 08-AUGUST-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BERKMAN, CHARLES S.
;             REGISTRATION NUMBER: 38,077
;             REFERENCE/DOCKET NUMBER: 227/166
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 619/552-2200
;             TELEFAX: 213/955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 35
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 39 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        FEATURE:
;             LOCATION:  39
;             OTHER INFORMATION:  amidated Ser (Serineamide)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-08-908-867-35

  Query Match             63.8%;  Score 71.5;  DB 13;  Length 39;
  Best Local Similarity   59.4%;  Pred. No. 1.3e-05;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDLSKQLEEEAVRLFIEFLKNGGASSGA 35


RESULT 8
```

```
US-09-003-869-171
; Sequence 171, Application US/09003869A
; GENERAL INFORMATION:
;  APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
;  APPLICANT: PRICKETT, KATHRYN S.
;  APPLICANT: BHAVSAR, SUNIL
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
;  TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
;  FILE REFERENCE: 231/181
;  CURRENT APPLICATION NUMBER: US/09/003,869A
;  CURRENT FILING DATE: 1998-01-07
;  EARLIER APPLICATION NUMBER: US 60/034,905
;  EARLIER FILING DATE: 1997-01-07
;  EARLIER APPLICATION NUMBER: US 60/055,404
;  EARLIER FILING DATE: 1997-08-08
;  EARLIER APPLICATION NUMBER: US 60/065,442
;  EARLIER FILING DATE: 1997-11-14
;  EARLIER APPLICATION NUMBER: US 60/066,029
;  EARLIER FILING DATE: 1997-11-14
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 171
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificially synthesized sequence of novel exendin agonist
;   OTHER INFORMATION: compound
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (36)...(36)
;   OTHER INFORMATION: amidated Pro (Prolinamide)
US-09-003-869-171

  Query Match             62.9%;  Score 70.5;  DB 14;  Length 36;
  Best Local Similarity   59.4%;  Pred. No. 1.8e-05;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 9
US-09-323-867A-171
; Sequence 171, Application US/09323867A
; GENERAL INFORMATION:
;  APPLICANT: Amylin Pharmaceuticals, Inc.
;  APPLICANT:  Young, Andrew et al.
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
;  TITLE OF INVENTION:  OF GESTATIONAL DIABETES MELLITUS
;  FILE REFERENCE: 030639.0032.UTL2 (243/131US)
;  CURRENT APPLICATION NUMBER: US/09/323,867A
;  CURRENT FILING DATE:  1999-06-01
;  NUMBER OF SEQ ID NOS: 189
;  SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 171
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificial sequence with specific variable residues
;   NAME/KEY: MOD_RES
;   LOCATION: (36)
;   OTHER INFORMATION: AMIDATION, Position 36 is Pro-NH2
US-09-323-867A-171

  Query Match             62.9%;  Score 70.5;  DB 17;  Length 36;
  Best Local Similarity   59.4%;  Pred. No. 1.8e-05;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
```

```
;   OTHER INFORMATION: naphthylalanine
;   NAME/KEY: VARIANT
;   LOCATION: (27)
;   OTHER INFORMATION: Xaa in position 27 is Lys-Asn-Lys, Lys-NH3-R-Asn,
;   OTHER INFORMATION: Asn-Lys-NH3-R where R is Lys, Arg, C1-C10 straight
;   OTHER INFORMATION: chain or branched alkanoyl or cycloalkylalkanoyl
;   NAME/KEY: VARIANT
;   LOCATION: (30)
;   OTHER INFORMATION: Xaa in position is independently Pro,
;   OTHER INFORMATION: homoproline, 3-hydroxproline, 4-hydroxyproline,
;   OTHER INFORMATION: thioproline, N-alkylglycine, N-alkylpentylglycine
;   OTHER INFORMATION: or N-alkylalanine
;   NAME/KEY: VARIANT
;   LOCATION: (35)..(39)
;   OTHER INFORMATION: Xaa in positions 35-39 is independently Pro,
;   OTHER INFORMATION: homoproline, 3-hydroxproline, 4-hydroxyproline,
;   OTHER INFORMATION: thioproline, N-alkylglycine, N-alkylpentylglycine
;   OTHER INFORMATION: or N-alkylalanine
;   NAME/KEY: VARIANT
;   LOCATION: (40)
;   OTHER INFORMATION: Xaa in position 40 is -OH or NH2, with the proviso
;   OTHER INFORMATION: that the compound does not have the formula of
;   OTHER INFORMATION: either SEQ. ID. NOS. 1 or 2
US-09-889-331-48

  Query Match             70.5%;  Score 79;  DB 22;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-07;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLXGGXSSGA 34
              |||||||||||||||||||||||||||||||
Db          4 GTXXXXXSKQXEEEAVRLXXXXLXGGXSSGA 34


RESULT 5
US-08-908-867-35
; Sequence 35, Application US/08908867
;  GENERAL INFORMATION:
;    APPLICANT:  YOUNG, Andrew A.
;    APPLICANT:  GEDULIN, Bronislava
;    APPLICANT:  BEELEY, Nigel Robert Arnold
;    APPLICANT:  PRICKETT, Kathryn S.
;    TITLE OF INVENTION:  METHODS FOR REGULATING
;    TITLE OF INVENTION:  GASTROINTESTINAL MOTIITY
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LYON & LYON
;      STREET:  633 WEST FIFTH STREET
;      CITY:  LOS ANGELES
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  90017
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/908,867
;      FILING DATE:  08-AUGUST-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/694,954
;      FILING DATE:  08-AUGUST-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DUFT, BRADFORD J.
;      REGISTRATION NUMBER:  32,219
;      REFERENCE/DOCKET NUMBER:  227/166
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/552-2200
;      TELEFAX:  213/955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      LOCATION:  31, 36, 37, 38
;      OTHER INFORMATION:  N-methylalanine
;      LOCATION:  39
;      OTHER INFORMATION:  amidated Ser (Serineamide)
US-08-908-867-35

  Query Match             63.8%;  Score 71.5;  DB 13;  Length 39;
  Best Local Similarity   59.4%;  Pred. No. 1.3e-05;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDLSKQLEEEAVRLFIEFLKNGGASSGA 35


RESULT 6
US-08-908-867A-35
; Sequence 35, Application US/08908867A
;  GENERAL INFORMATION:
;    APPLICANT:  YOUNG, Andrew A.
;    APPLICANT:  GEDULIN, Bronislava
;    APPLICANT:  BEELEY, Nigel Robert Arnold
;    APPLICANT:  PRICKETT, Kathryn S.
;    TITLE OF INVENTION:  METHODS FOR REGULATING
;    TITLE OF INVENTION:  GASTROINTESTINAL MOTILITY
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LYON & LYON
;      STREET:  633 WEST FIFTH STREET
;      CITY:  LOS ANGELES
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  90017
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/908,867A
;      FILING DATE:  08-AUGUST-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/694,954
;      FILING DATE:  08-AUGUST-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DUFT, BRADFORD J.
;      REGISTRATION NUMBER:  32,219
;      REFERENCE/DOCKET NUMBER:  227/166
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/552-2200
;      TELEFAX:  213/955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      LOCATION:  31, 36, 37, 38
;      OTHER INFORMATION:  N-methylalanine
;      LOCATION:  39
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;  CURRENT FILING DATE:  2000-04-28
;  PRIOR APPLICATION NUMBER: US 60/132,018
;  PRIOR FILING DATE: 1999-04-30
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: Microsoft Word and PatentIn 3.0
; SEQ ID NO 48
;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: synthetic construct
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)
;   OTHER INFORMATION: His, Arg, Tyr or 4-imidazopropionyl
;   NAME/KEY: VARIANT
;   LOCATION: (2)
;   OTHER INFORMATION: Ser, Gly, Ala or Thr
;   NAME/KEY: VARIANT
;   LOCATION: (3)
;   OTHER INFORMATION: Asp or Glu
;   NAME/KEY: VARIANT
;   LOCATION: (6)
;   OTHER INFORMATION: Phe, Tyr or naphthylalanine
;   NAME/KEY: VARIANT
;   LOCATION: (7)..(8)
;   OTHER INFORMATION: Thr or Ser
;   NAME/KEY: VARIANT
;   LOCATION: (9)
;   OTHER INFORMATION: Asp or Glu
;   NAME/KEY: VARIANT
;   LOCATION: (10)
;   OTHER INFORMATION: Leu, Ile, Val, pentylglycine or Met
;   NAME/KEY: VARIANT
;   LOCATION: (14)
;   OTHER INFORMATION: Leu, Ile, pentylglycine, Val or Met
;   NAME/KEY: VARIANT
;   LOCATION: (22)
;   OTHER INFORMATION: Phe, Tyr or naphthylalanine
;   NAME/KEY: VARIANT
;   LOCATION: (23)
;   OTHER INFORMATION: Ile, Val, Leu, pentylglycine, tert-butylglycine or Met
;   NAME/KEY: VARIANT
;   LOCATION: (24)
;   OTHER INFORMATION: Glu or Asp
;   NAME/KEY: VARIANT
;   LOCATION: (25)
;   OTHER INFORMATION: Trp, Phe, Tyr, or naphthylalanine
;   NAME/KEY: VARIANT
;   LOCATION: (27)
;   OTHER INFORMATION: Lys-Asn, Asn-Lys, Lys-NH3-R-Asn, Asn-Lys-NH3-R
;   OTHER INFORMATION: where R is Lys, Arg, C1-C10 straight chain or
;   OTHER INFORMATION: branched alkanoyl or cycloalkylalkanoyl
;   NAME/KEY: VARIANT
;   LOCATION: (30)
;   OTHER INFORMATION: independently Pro, homoproline, 3-hydroxyproline,
;   OTHER INFORMATION: 4-hydroxyproline, thioproline, N-alkylglycine,
;   OTHER INFORMATION: N-alkylpentylglycine or N-alkylalanine
;   NAME/KEY: VARIANT
;   LOCATION: (36)..(38)
;   OTHER INFORMATION: independently Pro, homoproline, 3-hydroxyproline,
;   OTHER INFORMATION: 4-hydroxyproline, thioproline, N-alkylglycine,
;   OTHER INFORMATION: N-alkylpentylglycine or N-alkylalanine
;   NAME/KEY: VARIANT
;   LOCATION: (39)
;   OTHER INFORMATION: Ser Thr or Tyr
;   NAME/KEY: VARIANT
;   LOCATION: (40)
;   OTHER INFORMATION: OH or NH2, with the proviso that the compound does
;   OTHER INFORMATION: not have the formula of either SEQ. ID. NOS. 1 or 2.
US-09-561-226-48

  Query Match             70.5%;  Score 79;  DB 19;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-07;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLXGGXSSGA 34
              |||||||||||||||||||||||||||||||
Db          4 GTXXXXXSKQXEEEAVRLXXXXLXGGXSSGA 34


RESULT 4
US-09-889-331-48
; Sequence 48, Application US/09889331
; GENERAL INFORMATION:
;  APPLICANT: YOUNG, ANDREW A.
;  APPLICANT:  GEDULIN, BRONISLAVA
;  TITLE OF INVENTION: METHODS FOR GLUCAGON SUPPRESSION
;  FILE REFERENCE: 030639.0031.UTL1 (249/167)
;  CURRENT APPLICATION NUMBER: US/09/889,331
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: PCT/US00/00942
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 60/116,380
;  PRIOR FILING DATE: 1999-01-14
;  PRIOR APPLICATION NUMBER: 60/132,017
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 239
;  SOFTWARE: FastSEQ for Windows Version 4.0, Microsoft WORD 97 SR-2
; SEQ ID NO 48
;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Construct
;   NAME/KEY: VARIANT
;   LOCATION: (1)
;   OTHER INFORMATION: Xaa in position 1 is His, Arg, Tyr or
;   OTHER INFORMATION: 4-imidazopropionyl
;   NAME/KEY: VARIANT
;   LOCATION: (2)
;   OTHER INFORMATION: Xaa in position 2 is Ser, Gly, Ala or Thr
;   NAME/KEY: VARIANT
;   LOCATION: (3)
;   OTHER INFORMATION: Xaa in position 3 is Asp or Glu
;   NAME/KEY: VARIANT
;   LOCATION: (6)
;   OTHER INFORMATION: Xaa in position 6 is Phe, Tyr or naphthylalanine
;   NAME/KEY: VARIANT
;   LOCATION: (7)..(8)
;   OTHER INFORMATION: Xaa in positions 7 & 8 is Thr or Ser
;   NAME/KEY: VARIANT
;   LOCATION: (9)
;   OTHER INFORMATION: Xaa in position 9 is Asp or Glu
;   NAME/KEY: VARIANT
;   LOCATION: (10)
;   OTHER INFORMATION: Xaa in position 10 is Leu, Ile, Val, pentylglycine
;   OTHER INFORMATION: or Met
;   NAME/KEY: VARIANT
;   LOCATION: (14)
;   OTHER INFORMATION: Xaa at position 14 is Leu, Ile, pentylglycine,
;   OTHER INFORMATION: Val or Met
;   NAME/KEY: VARIANT
;   LOCATION: (22)
;   OTHER INFORMATION: Xaa in position 22 is Phe, Tyr or naphthylalanine
;   NAME/KEY: VARIANT
;   LOCATION: (23)
;   OTHER INFORMATION: Xaa in position 23 is Ile, Val, Lu, pentylglycine,
;   OTHER INFORMATION: tert-butylglycine or Met
;   NAME/KEY: VARIANT
;   LOCATION: (24)
;   OTHER INFORMATION: Xaa in position 24 is Glu or Asp
;   NAME/KEY: VARIANT
;   LOCATION: (25)
;   OTHER INFORMATION: Xaa in position 25 is Trp, Phe, Tyr, or
```

```
;   OTHER INFORMATION: Xaa in position 3 stands for Asp or Glu
;   NAME/KEY: VARIANT
;   LOCATION: 6
;   OTHER INFORMATION: Xaa in position 6 stands for Phe, Tyr or
;   OTHER INFORMATION: naphthylalanine
;   NAME/KEY: VARIANT
;   LOCATION: 7, 8
;   OTHER INFORMATION: Xaa in positions 7-8 stands for Thr or Ser
;   NAME/KEY: VARIANT
;   LOCATION: 10, 14
;   OTHER INFORMATION: Xaa in positions 10 and 14 stands for Leu, Ile,
;   OTHER INFORMATION: Val, pentylglycine or Met
;   NAME/KEY: VARIANT
;   LOCATION: 22
;   OTHER INFORMATION: Xaa in position 22 stands for Phe, Tyr or
;   OTHER INFORMATION: naphthylalanine
;   NAME/KEY: VARIANT
;   LOCATION: 23
;   OTHER INFORMATION: Xaa in position 23 stands for Ile, Val, Leu,
;   OTHER INFORMATION: pentylglycine, tert-butylglycine or Met
;   NAME/KEY: VARIANT
;   LOCATION: 24
;   OTHER INFORMATION: Xaa in position 24 stands for Glu or Asp
;   NAME/KEY: VARIANT
;   LOCATION: 25
;   OTHER INFORMATION: Xaa in position 25 stands for Trp, Phe, Tyr or
;   OTHER INFORMATION: naphthylalanine
;   NAME/KEY: VARIANT
;   LOCATION: 27
;   OTHER INFORMATION: Xaa in position 27 stands for Lys Asn, Asn Lys,
;   OTHER INFORMATION: Lys-NH(epsilon)-R Asn, Asn Lys-NH3-R where R is Lys,
;   OTHER INFORMATION: Arg, C1-C10 straight chain or branched alkanoyl or
;   OTHER INFORMATION: cycloalkylalkanoyl
;   NAME/KEY: VARIANT
;   LOCATION: 30, 35-37
;   OTHER INFORMATION: Xaa in positions 30, 35-37 are selected from Pro,
;   OTHER INFORMATION: homoproline, 3Hyp, 4Hyp, thioproline,
;   OTHER INFORMATION: N-alkylglycine, N-alkylpentylglycine or
;   OTHER INFORMATION: N-alkylalanine
;   NAME/KEY: VARIANT
;   LOCATION: 39
;   OTHER INFORMATION: Xaa in position 38 stands for Ser, Thr or Tyr and
;   OTHER INFORMATION: is optionally amidated
US-09-561-226A-210

  Query Match            70.5%;  Score 79;  DB 19;  Length 38;
  Best Local Similarity  100.0%;  Pred. No. 4.7e-07;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLXGGXSSGA 34
              |||||||||||||||||||||||||||||||
Db          4 GTXXXXXSKQXEEEAVRLXXXXLXGGXSSGA 34


RESULT 2
US-09-561-226D-210
; Sequence 210, Application US/09561226D
; GENERAL INFORMATION:
;  APPLICANT: Prickett, Kathryn S
;  APPLICANT:  Young, Andrew A
;  TITLE OF INVENTION: MODIFIED EXENDINS AND EXENDIN AGONISTS
;  FILE REFERENCE: 030639.0028.UTL(253/204)
;  CURRENT APPLICATION NUMBER: US/09/561,226D
;  CURRENT FILING DATE:  2000-04-28
;  PRIOR APPLICATION NUMBER: 60/132,018
;  PRIOR FILING DATE: 1999-04-30
;  NUMBER OF SEQ ID NOS: 240
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 210
;   LENGTH: 38
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Amino Acid Sequence
;   NAME/KEY: VARIANT
;   LOCATION: 1
;   OTHER INFORMATION: Xaa in position 1 stands for His, Arg, Tyr or
;   OTHER INFORMATION: 4-Imidazopropionyl
;   NAME/KEY: VARIANT
;   LOCATION: 2
;   OTHER INFORMATION: Xaa in position 2 stands for Ser, Gly, Ala or Thr
;   NAME/KEY: VARIANT
;   LOCATION: 3, 9
;   OTHER INFORMATION: Xaa in position 3 stands for Asp or Glu
;   NAME/KEY: VARIANT
;   LOCATION: 6
;   OTHER INFORMATION: Xaa in position 6 stands for Phe, Tyr or
;   OTHER INFORMATION: naphthylalanine
;   NAME/KEY: VARIANT
;   LOCATION: 7, 8
;   OTHER INFORMATION: Xaa in positions 7-8 stands for Thr or Ser
;   NAME/KEY: VARIANT
;   LOCATION: 10, 14
;   OTHER INFORMATION: Xaa in positions 10 and 14 stands for Leu, Ile,
;   OTHER INFORMATION: Val, pentylglycine or Met
;   NAME/KEY: VARIANT
;   LOCATION: 22
;   OTHER INFORMATION: Xaa in position 22 stands for Phe, Tyr or
;   OTHER INFORMATION: naphthylalanine
;   NAME/KEY: VARIANT
;   LOCATION: 23
;   OTHER INFORMATION: Xaa in position 23 stands for Ile, Val, Leu,
;   OTHER INFORMATION: pentylglycine, tert-butylglycine or Met
;   NAME/KEY: VARIANT
;   LOCATION: 24
;   OTHER INFORMATION: Xaa in position 24 stands for Glu or Asp
;   NAME/KEY: VARIANT
;   LOCATION: 25
;   OTHER INFORMATION: Xaa in position 25 stands for Trp, Phe, Tyr or
;   OTHER INFORMATION: naphthylalanine
;   NAME/KEY: VARIANT
;   LOCATION: 27
;   OTHER INFORMATION: Xaa in position 27 stands for Lys Asn, Asn Lys,
;   OTHER INFORMATION: Lys-NH(epsilon)-R Asn, Asn Lys-NH3-R where R is Lys,
;   OTHER INFORMATION: Arg, C1-C10 straight chain or branched alkanoyl or
;   OTHER INFORMATION: cycloalkylalkanoyl
;   NAME/KEY: VARIANT
;   LOCATION: 30, 35-37
;   OTHER INFORMATION: Xaa in positions 30, 35-37 are selected from Pro,
;   OTHER INFORMATION: homoproline, 3Hyp, 4Hyp, thioproline,
;   OTHER INFORMATION: N-alkylglycine, N-alkylpentylglycine or
;   OTHER INFORMATION: N-alkylalanine
;   NAME/KEY: VARIANT
;   LOCATION: 39
;   OTHER INFORMATION: Xaa in position 38 stands for Ser, Thr or Tyr and
;   OTHER INFORMATION: is optionally amidated
US-09-561-226D-210

  Query Match            70.5%;  Score 79;  DB 19;  Length 38;
  Best Local Similarity  100.0%;  Pred. No. 4.7e-07;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLXGGXSSGA 34
              |||||||||||||||||||||||||||||||
Db          4 GTXXXXXSKQXEEEAVRLXXXXLXGGXSSGA 34


RESULT 3
US-09-561-226-48
; Sequence 48, Application US/09561226
; GENERAL INFORMATION:
;  APPLICANT: Amylin Pharmaceuticals, Inc.
;  APPLICANT:  Young, Andrew
;  TITLE OF INVENTION: MODIFIED EXENDINS AND EXENDIN AGONISTS
;  FILE REFERENCE: 253/204 US Amylin
;  CURRENT APPLICATION NUMBER: US/09/561,226
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 24, 2003, 23:05:25 ; Search time 221 Seconds
(without alignments)
116.694 Million cell updates/sec

Title: US-09-889-331A-48
Perfect score: 112
Sequence: 1 XXXGTXXXXXSKQXEEEAVRLXXXXLXGGXSSGAXXXXXX 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*
1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US080_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US082_COMB.pep:*
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8: /cgn2_6/ptodata/1/paa/US084_COMB.pep:*
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11: /cgn2_6/ptodata/1/paa/US087_COMB.pep:*
12: /cgn2_6/ptodata/1/paa/US088_COMB.pep:*
13: /cgn2_6/ptodata/1/paa/US089_COMB.pep:*
14: /cgn2_6/ptodata/1/paa/US090_COMB.pep:*
15: /cgn2_6/ptodata/1/paa/US091_COMB.pep:*
16: /cgn2_6/ptodata/1/paa/US092_COMB.pep:*
17: /cgn2_6/ptodata/1/paa/US093_COMB.pep:*
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19: /cgn2_6/ptodata/1/paa/US095_COMB.pep:*
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27: /cgn2_6/ptodata/1/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	79	70.5	38	19	US-09-561-226A-210	Sequence 210, App
2	79	70.5	38	19	US-09-561-226D-210	Sequence 210, App
3	79	70.5	40	19	US-09-561-226-48	Sequence 48, Appl
4	79	70.5	40	22	US-09-889-331-48	Sequence 48, Appl
5	71.5	63.8	39	13	US-08-908-867-35	Sequence 35, Appl
6	71.5	63.8	39	13	US-08-908-867A-35	Sequence 35, Appl
7	71.5	63.8	39	13	US-08-908-867-35	Sequence 35, Appl
8	70.5	62.9	36	14	US-09-003-869-171	Sequence 171, App
9	70.5	62.9	36	17	US-09-323-867A-171	Sequence 171, App
10	70.5	62.9	36	19	US-09-561-226A-166	Sequence 166, App
11	70.5	62.9	36	19	US-09-561-226D-166	Sequence 166, App
12	70.5	62.9	36	21	US-09-756-690A-171	Sequence 171, App
13	70.5	62.9	36	22	US-09-889-331-189	Sequence 189, App
14	70.5	62.9	36	23	US-09-554-531A-76	Sequence 76, Appl
15	70.5	62.9	37	14	US-09-003-869-99	Sequence 99, Appl
16	70.5	62.9	37	14	US-09-003-869-183	Sequence 183, App
17	70.5	62.9	37	17	US-09-323-867A-99	Sequence 99, Appl
18	70.5	62.9	37	17	US-09-323-867A-183	Sequence 183, App
19	70.5	62.9	37	19	US-09-561-226A-86	Sequence 86, Appl
20	70.5	62.9	37	19	US-09-561-226A-178	Sequence 178, App
21	70.5	62.9	37	19	US-09-561-226D-86	Sequence 86, Appl
22	70.5	62.9	37	19	US-09-561-226D-178	Sequence 178, App
23	70.5	62.9	37	20	US-09-622-105-65	Sequence 65, Appl
24	70.5	62.9	37	21	US-09-756-690A-99	Sequence 99, Appl
25	70.5	62.9	37	21	US-09-756-690A-183	Sequence 183, App
26	70.5	62.9	37	22	US-09-889-331-109	Sequence 109, App
27	70.5	62.9	37	22	US-09-889-331-201	Sequence 201, App
28	70.5	62.9	37	23	US-09-554-531A-88	Sequence 88, Appl
29	70.5	62.9	39	13	US-08-908-867-33	Sequence 33, Appl
30	70.5	62.9	39	13	US-08-908-867A-33	Sequence 33, Appl
31	70.5	62.9	39	13	US-08-908-867-33	Sequence 33, Appl
32	70.5	62.9	39	14	US-09-003-869-35	Sequence 35, Appl
33	70.5	62.9	39	14	US-09-003-869-36	Sequence 36, Appl
34	70.5	62.9	39	14	US-09-003-869-39	Sequence 39, Appl
35	70.5	62.9	39	17	US-09-323-867A-35	Sequence 35, Appl
36	70.5	62.9	39	17	US-09-323-867A-36	Sequence 36, Appl
37	70.5	62.9	39	17	US-09-323-867A-39	Sequence 39, Appl
38	70.5	62.9	39	19	US-09-561-226-36	Sequence 36, Appl
39	70.5	62.9	39	19	US-09-561-226-37	Sequence 37, Appl
40	70.5	62.9	39	19	US-09-561-226-40	Sequence 40, Appl
41	70.5	62.9	39	21	US-09-756-690A-35	Sequence 35, Appl
42	70.5	62.9	39	21	US-09-756-690A-36	Sequence 36, Appl
43	70.5	62.9	39	21	US-09-756-690A-39	Sequence 39, Appl
44	70.5	62.9	39	22	US-09-889-331-36	Sequence 36, Appl
45	70.5	62.9	39	22	US-09-889-331-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-09-561-226A-210
; Sequence 210, Application US/09561226A
; GENERAL INFORMATION:
; APPLICANT: Prickett, Kathryn S
; APPLICANT: Young, Andrew A
; TITLE OF INVENTION: MODIFIED EXENDINS AND EXENDIN AGONISTS
; FILE REFERENCE: 030639.0028.UTL(253/204)
; CURRENT APPLICATION NUMBER: US/09/561,226A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/132,018
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 210
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Amino Acid Sequence
; NAME/KEY: VARIANT
; LOCATION: 1
; OTHER INFORMATION: Xaa in position 1 stands for His, Arg, Tyr or
; OTHER INFORMATION: 4-Imidazopropionyl
; NAME/KEY: VARIANT
; LOCATION: 2
; OTHER INFORMATION: Xaa in position 2 stands for Ser, Gly, Ala or Thr
; NAME/KEY: VARIANT
; LOCATION: 3, 9

```
; SEQ ID NO 99
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
;   FEATURE:
;   OTHER INFORMATION: c-term amidation
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (31)
;   OTHER INFORMATION: Homoproline
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (36)..(37)
;   OTHER INFORMATION: Homoproline
US-10-157-224A-99

  Query Match             62.9%;  Score 70.5;  DB 6;  Length 37;
  Best Local Similarity   62.5%;  Pred. No. 2.3e-06;
  Matches   20;  Conservative    0;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  |||||||
Db          4 GTFTSDASKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 14
US-10-157-224A-183
; Sequence 183, Application US/10157224A
; GENERAL INFORMATION:
;  APPLICANT: YOUNG, ANDREW A.
;  APPLICANT:  KOLTERMAN, ORVILLE G.
;  TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
;  TITLE OF INVENTION:  ADMINISTRATION THEREOF
;  FILE REFERENCE: 02001-050
;  CURRENT APPLICATION NUMBER: US/10/157,224A
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: 09/889,330
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: PCT/US00/00902
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 60/116,380
;  PRIOR FILING DATE: 1999-01-14
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 183
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
;   FEATURE:
;   OTHER INFORMATION: c-term amidation
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (31)
;   OTHER INFORMATION: N-methylalanine
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (36)..(37)
;   OTHER INFORMATION: N-methylalanine
US-10-157-224A-183

  Query Match             62.9%;  Score 70.5;  DB 6;  Length 37;
  Best Local Similarity   62.5%;  Pred. No. 2.3e-06;
  Matches   20;  Conservative    0;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  |||||||
Db          4 GTFTSALSKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 15
US-10-342-014-99
; Sequence 99, Application US/10342014
; GENERAL INFORMATION:
;  APPLICANT: Amylin Pharmaceuticals, Inc.
;  APPLICANT:  Hiles, Richard A. et al.
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
;  TITLE OF INVENTION:  OF GESTATIONAL DIABETES MELLITUS
;  FILE REFERENCE: 18528.169 (0204-CON-0)
;  CURRENT APPLICATION NUMBER: US/10/342,014
;  CURRENT FILING DATE:  2003-01-13
;  PRIOR APPLICATION NUMBER: 09/323,867
;  PRIOR FILING DATE: 1999-06-01
;  NUMBER OF SEQ ID NOS: 189
;  SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 99
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificial sequence with specific variable residues
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (31)
;   OTHER INFORMATION: Xaa is homoproline
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (36)..(37)
;   OTHER INFORMATION: Xaa is homoproline
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (37)
;   OTHER INFORMATION: AMIDATION, Position 37 is homoproline-NH2
US-10-342-014-99

  Query Match             62.9%;  Score 70.5;  DB 6;  Length 37;
  Best Local Similarity   62.5%;  Pred. No. 2.3e-06;
  Matches   20;  Conservative    0;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  |||||||
Db          4 GTFTSDASKQMEEEAVRLFIEWLKNGGXSSGA 35


Search completed: June 24, 2003, 23:19:19
Job time : 72.5 secs
```

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;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Amino Acid Sequence
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (31)
;   OTHER INFORMATION: Xaa in position 31 stands for Nme
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (36)..(37)
;   OTHER INFORMATION: Xaa in positions 36-37 stands for Nme
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (37)
;   OTHER INFORMATION: Nme in position 37 is amidated
US-09-889-331A-201

  Query Match             62.9%;  Score 70.5;  DB 5;  Length 37;
  Best Local Similarity   62.5%;  Pred. No. 2.3e-06;
  Matches   20;  Conservative    0;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  |||||||
Db          4 GTFTSALSKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 11
US-10-187-051-99
; Sequence 99, Application US/10187051
; GENERAL INFORMATION:
;  APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
;  APPLICANT:  PRICKETT, KATHRYN S.
;  APPLICANT:  BHAVSAR, SUNIL
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
;  TITLE OF INVENTION:  THE REDUCTION OF FOOD INTAKE
;  FILE REFERENCE: 231/181
;  CURRENT APPLICATION NUMBER: US/10/187,051
;  CURRENT FILING DATE:  2002-06-28
;  PRIOR APPLICATION NUMBER: US/09/003,869
;  PRIOR FILING DATE: 1998-01-07
;  PRIOR APPLICATION NUMBER: US 60/034,905
;  PRIOR FILING DATE: 1997-01-07
;  PRIOR APPLICATION NUMBER: US 60/055,404
;  PRIOR FILING DATE: 1997-08-08
;  PRIOR APPLICATION NUMBER: US 60/065,442
;  PRIOR FILING DATE: 1997-11-14
;  PRIOR APPLICATION NUMBER: US 60/066,029
;  PRIOR FILING DATE: 1997-11-14
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 99
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificially synthesized sequence of novel exendin
;   OTHER INFORMATION: agonist
;   OTHER INFORMATION: compound
;   FEATURE:
;   OTHER INFORMATION: Xaa in positions 31, 36 and 37 stands for homoproline.
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (37)...(37)
;   OTHER INFORMATION: amidated hPro (homoprolinamide)
US-10-187-051-99

  Query Match             62.9%;  Score 70.5;  DB 6;  Length 37;
  Best Local Similarity   62.5%;  Pred. No. 2.3e-06;
  Matches   20;  Conservative    0;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  |||||||
Db          4 GTFTSDASKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 12
US-10-187-051-183
; Sequence 183, Application US/10187051
; GENERAL INFORMATION:
;  APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
;  APPLICANT:  PRICKETT, KATHRYN S.
;  APPLICANT:  BHAVSAR, SUNIL
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
;  TITLE OF INVENTION:  THE REDUCTION OF FOOD INTAKE
;  FILE REFERENCE: 231/181
;  CURRENT APPLICATION NUMBER: US/10/187,051
;  CURRENT FILING DATE:  2002-06-28
;  PRIOR APPLICATION NUMBER: US/09/003,869
;  PRIOR FILING DATE: 1998-01-07
;  PRIOR APPLICATION NUMBER: US 60/034,905
;  PRIOR FILING DATE: 1997-01-07
;  PRIOR APPLICATION NUMBER: US 60/055,404
;  PRIOR FILING DATE: 1997-08-08
;  PRIOR APPLICATION NUMBER: US 60/065,442
;  PRIOR FILING DATE: 1997-11-14
;  PRIOR APPLICATION NUMBER: US 60/066,029
;  PRIOR FILING DATE: 1997-11-14
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 183
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificially synthesized sequence of novel exendin
;   OTHER INFORMATION: agonist
;   OTHER INFORMATION: compound
;   FEATURE:
;   OTHER INFORMATION: Xaa in positions 31, 36 and 37 stands for n-
;   OTHER INFORMATION: methylalanine.
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (37)...(37)
;   OTHER INFORMATION: amidated Nmeala (n-methylalaninamide)
US-10-187-051-183

  Query Match             62.9%;  Score 70.5;  DB 6;  Length 37;
  Best Local Similarity   62.5%;  Pred. No. 2.3e-06;
  Matches   20;  Conservative    0;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  |||||||
Db          4 GTFTSALSKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 13
US-10-157-224A-99
; Sequence 99, Application US/10157224A
; GENERAL INFORMATION:
;  APPLICANT: YOUNG, ANDREW A.
;  APPLICANT:  KOLTERMAN, ORVILLE G.
;  TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
;  TITLE OF INVENTION:  ADMINISTRATION THEREOF
;  FILE REFERENCE: 02001-050
;  CURRENT APPLICATION NUMBER: US/10/157,224A
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: 09/889,330
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: PCT/US00/00902
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 60/116,380
;  PRIOR FILING DATE: 1999-01-14
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: PatentIn Ver. 2.1
```

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;   FEATURE:
;   OTHER INFORMATION: artificial sequence with specific variable residues
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (31)
;   OTHER INFORMATION: Xaa is homoproline
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (36)..(37)
;   OTHER INFORMATION: Xaa is homoproline
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (37)
;   OTHER INFORMATION: AMIDATION, Position 37 is homoproline-NH2
PCT-US03-16699-99

  Query Match             62.9%;  Score 70.5;  DB 1;  Length 37;
  Best Local Similarity   62.5%;  Pred. No. 2.3e-06;
  Matches   20;  Conservative    0;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  |||||||
Db          4 GTFTSDASKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 8
PCT-US03-16699-183
; Sequence 183, Application PC/TUS0316699
; GENERAL INFORMATION:
;  APPLICANT: Amylin Pharmaceuticals, Inc.
;  APPLICANT:  Young, Andrew A. et al.
;  TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF ADMINISTRATIO T
;  FILE REFERENCE: 18528.464 (0201-CIP-5)
;  CURRENT APPLICATION NUMBER: PCT/US03/16699
;  CURRENT FILING DATE:  2003-05-28
;  PRIOR APPLICATION NUMBER: 10/157,224
;  PRIOR FILING DATE: 2002-05-28
;  PRIOR APPLICATION NUMBER: <NOT YET ASSIGNED>
;  PRIOR FILING DATE: 2002-05-28
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 183
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificial sequence with specific variable residues
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (31)
;   OTHER INFORMATION: Xaa is N-methylalanine
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (36)..(37)
;   OTHER INFORMATION: Xaa is N-methylalanine
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (37)
;   OTHER INFORMATION: AMIDATION, Position 37 is N-methylalanine-NH2
PCT-US03-16699-183

  Query Match             62.9%;  Score 70.5;  DB 1;  Length 37;
  Best Local Similarity   62.5%;  Pred. No. 2.3e-06;
  Matches   20;  Conservative    0;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  |||||||
Db          4 GTFTSALSKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 9
US-09-889-331A-109
; Sequence 109, Application US/09889331A
; GENERAL INFORMATION:
;  APPLICANT: YOUNG, ANDREW A.
;  APPLICANT:  GEDULIN, BRONISLAVA
;  TITLE OF INVENTION: METHODS FOR GLUCAGON SUPPRESSION
;  FILE REFERENCE: 030639.0031.UTL1 (249/167)
;  CURRENT APPLICATION NUMBER: US/09/889,331A
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: PCT/US00/00942
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 60/116,380
;  PRIOR FILING DATE: 1999-01-14
;  PRIOR APPLICATION NUMBER: 60/132,017
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 239
;  SOFTWARE: FastSEQ for Windows Version 4.0
;    Microsoft WORD 97 SR-2
; SEQ ID NO 109
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Amino Acid Sequence
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (31)
;   OTHER INFORMATION: Xaa in position 31 stands for hPro
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (36)..(37)
;   OTHER INFORMATION: Xaa in positions 36-37 stands for hPro
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (37)
;   OTHER INFORMATION: hPro in position 37 is amidated
US-09-889-331A-109

  Query Match             62.9%;  Score 70.5;  DB 5;  Length 37;
  Best Local Similarity   62.5%;  Pred. No. 2.3e-06;
  Matches   20;  Conservative    0;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  |||||||
Db          4 GTFTSDASKQMEEEAVRLFIEWLKNGGXSSGA 35


RESULT 10
US-09-889-331A-201
; Sequence 201, Application US/09889331A
; GENERAL INFORMATION:
;  APPLICANT: YOUNG, ANDREW A.
;  APPLICANT:  GEDULIN, BRONISLAVA
;  TITLE OF INVENTION: METHODS FOR GLUCAGON SUPPRESSION
;  FILE REFERENCE: 030639.0031.UTL1 (249/167)
;  CURRENT APPLICATION NUMBER: US/09/889,331A
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: PCT/US00/00942
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 60/116,380
;  PRIOR FILING DATE: 1999-01-14
;  PRIOR APPLICATION NUMBER: 60/132,017
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 239
;  SOFTWARE: FastSEQ for Windows Version 4.0
;    Microsoft WORD 97 SR-2
; SEQ ID NO 201
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
```

```
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 4
US-10-187-051-171
; Sequence 171, Application US/10187051
; GENERAL INFORMATION:
;  APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
;  APPLICANT:  PRICKETT, KATHRYN S.
;  APPLICANT:  BHAVSAR, SUNIL
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
;  TITLE OF INVENTION:  THE REDUCTION OF FOOD INTAKE
;  FILE REFERENCE: 231/181
;  CURRENT APPLICATION NUMBER: US/10/187,051
;  CURRENT FILING DATE:  2002-06-28
;  PRIOR APPLICATION NUMBER: US/09/003,869
;  PRIOR FILING DATE: 1998-01-07
;  PRIOR APPLICATION NUMBER: US 60/034,905
;  PRIOR FILING DATE: 1997-01-07
;  PRIOR APPLICATION NUMBER: US 60/055,404
;  PRIOR FILING DATE: 1997-08-08
;  PRIOR APPLICATION NUMBER: US 60/065,442
;  PRIOR FILING DATE: 1997-11-14
;  PRIOR APPLICATION NUMBER: US 60/066,029
;  PRIOR FILING DATE: 1997-11-14
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 171
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificially synthesized sequence of novel exendin
;   OTHER INFORMATION: agonist
;   OTHER INFORMATION: compound
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (36)...(36)
;   OTHER INFORMATION: amidated Pro (Prolinamide)
US-10-187-051-171

  Query Match             62.9%;  Score 70.5;  DB 6;  Length 36;
  Best Local Similarity   59.4%;  Pred. No. 2.2e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 5
US-10-157-224A-171
; Sequence 171, Application US/10157224A
; GENERAL INFORMATION:
;  APPLICANT: YOUNG, ANDREW A.
;  APPLICANT:  KOLTERMAN, ORVILLE G.
;  TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
;  TITLE OF INVENTION:  ADMINISTRATION THEREOF
;  FILE REFERENCE: 02001-050
;  CURRENT APPLICATION NUMBER: US/10/157,224A
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: 09/889,330
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: PCT/US00/00902
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 60/116,380
;  PRIOR FILING DATE: 1999-01-14
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 171
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
;   FEATURE:
;   OTHER INFORMATION: c-term amidation
US-10-157-224A-171

  Query Match             62.9%;  Score 70.5;  DB 6;  Length 36;
  Best Local Similarity   59.4%;  Pred. No. 2.2e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 6
US-10-342-014-171
; Sequence 171, Application US/10342014
; GENERAL INFORMATION:
;  APPLICANT: Amylin Pharmaceuticals, Inc.
;  APPLICANT:  Hiles, Richard A. et al.
;  TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
;  TITLE OF INVENTION:  OF GESTATIONAL DIABETES MELLITUS
;  FILE REFERENCE: 18528.169 (0204-CON-0)
;  CURRENT APPLICATION NUMBER: US/10/342,014
;  CURRENT FILING DATE:  2003-01-13
;  PRIOR APPLICATION NUMBER: 09/323,867
;  PRIOR FILING DATE: 1999-06-01
;  NUMBER OF SEQ ID NOS: 189
;  SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 171
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificial sequence with specific variable residues
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (36)
;   OTHER INFORMATION: AMIDATION, Position 36 is Pro-NH2
US-10-342-014-171

  Query Match             62.9%;  Score 70.5;  DB 6;  Length 36;
  Best Local Similarity   59.4%;  Pred. No. 2.2e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 7
PCT-US03-16699-99
; Sequence 99, Application PC/TUS0316699
; GENERAL INFORMATION:
;  APPLICANT: Amylin Pharmaceuticals, Inc.
;  APPLICANT:  Young, Andrew A. et al.
;  TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF ADMINISTRATI
;  FILE REFERENCE: 18528.464 (0201-CIP-5)
;  CURRENT APPLICATION NUMBER: PCT/US03/16699
;  CURRENT FILING DATE:  2003-05-28
;  PRIOR APPLICATION NUMBER: 10/157,224
;  PRIOR FILING DATE: 2002-05-28
;  PRIOR APPLICATION NUMBER: <NOT YET ASSIGNED>
;  PRIOR FILING DATE: 2002-05-28
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 99
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
```

```
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (9)
;   OTHER INFORMATION: Xaa in position 9 is Asp or Glu
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (10)
;   OTHER INFORMATION: Xaa in position 10 is Leu, Ile, Val, pentylglycine
;   OTHER INFORMATION: or Met
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (14)
;   OTHER INFORMATION: Xaa at position 14 is Leu, Ile, pentylglycine,
;   OTHER INFORMATION: Val or Met
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (22)
;   OTHER INFORMATION: Xaa in position 22 is Phe, Tyr or naphthylalanine
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (23)
;   OTHER INFORMATION: Xaa in position 23 is Ile, Val, Lu, pentylglycine,
;   OTHER INFORMATION: tert-butylglycine or Met
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (24)
;   OTHER INFORMATION: Xaa in position 24 is Glu or Asp
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (25)
;   OTHER INFORMATION: Xaa in position 25 is Trp, Phe, Tyr, or
;   OTHER INFORMATION: naphthylalanine
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (27)
;   OTHER INFORMATION: Xaa in position 27 is Lys-Asn-Lys, Lys-NH3-R-Asn,
;   OTHER INFORMATION: Asn-Lys-NH3-R where R is Lys, Arg, C1-C10 straight
;   OTHER INFORMATION: chain or branched alkanoyl or cycloalkylalkanoyl
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (30)
;   OTHER INFORMATION: Xaa in position is independently Pro,
;   OTHER INFORMATION: homoproline, 3-hydroxproline, 4-hydroxyproline,
;   OTHER INFORMATION: thioproline, N-alkylglycine, N-alkylpentylglycine
;   OTHER INFORMATION: or N-alkylalanine
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (35)..(39)
;   OTHER INFORMATION: Xaa in positions 35-39 is independently Pro,
;   OTHER INFORMATION: homoproline, 3-hydroxproline, 4-hydroxyproline,
;   OTHER INFORMATION: thioproline, N-alkylglycine, N-alkylpentylglycine
;   OTHER INFORMATION: or N-alkylalanine
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (40)
;   OTHER INFORMATION: Xaa in position 40 is -OH or NH2, with the proviso
;   OTHER INFORMATION: that the compound does not have the formula of
;   OTHER INFORMATION: either SEQ. ID. NOS. 1 or 2
US-09-889-331A-48

  Query Match             70.5%;  Score 79;  DB 5;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-08;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLXGGXSSGA 34
              |||||||||||||||||||||||||||||||
Db          4 GTXXXXXSKQXEEEAVRLXXXXLXGGXSSGA 34


RESULT 2
PCT-US03-16699-171
; Sequence 171, Application PC/TUS0316699
; GENERAL INFORMATION:
;  APPLICANT: Amylin Pharmaceuticals, Inc.
;  APPLICANT:  Young, Andrew A. et al.
;  TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF ADMINISTRATI
;  FILE REFERENCE: 18528.464 (0201-CIP-5)
;  CURRENT APPLICATION NUMBER: PCT/US03/16699
;  CURRENT FILING DATE:  2003-05-28
;  PRIOR APPLICATION NUMBER: 10/157,224
;  PRIOR FILING DATE: 2002-05-28
;  PRIOR APPLICATION NUMBER: <NOT YET ASSIGNED>
;  PRIOR FILING DATE: 2002-05-28
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
; SEQ ID NO 171
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificial sequence with specific variable residues
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (36)
;   OTHER INFORMATION: AMIDATION, Position 36 is Pro-NH2
PCT-US03-16699-171

  Query Match             62.9%;  Score 70.5;  DB 1;  Length 36;
  Best Local Similarity   59.4%;  Pred. No. 2.2e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35


RESULT 3
US-09-889-331A-189
; Sequence 189, Application US/09889331A
; GENERAL INFORMATION:
;  APPLICANT: YOUNG, ANDREW A.
;  APPLICANT:  GEDULIN, BRONISLAVA
;  TITLE OF INVENTION: METHODS FOR GLUCAGON SUPPRESSION
;  FILE REFERENCE: 030639.0031.UTL1 (249/167)
;  CURRENT APPLICATION NUMBER: US/09/889,331A
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: PCT/US00/00942
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 60/116,380
;  PRIOR FILING DATE: 1999-01-14
;  PRIOR APPLICATION NUMBER: 60/132,017
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 239
;  SOFTWARE: FastSEQ for Windows Version 4.0
;    Microsoft WORD 97 SR-2
; SEQ ID NO 189
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Amino Acid Sequence
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (36)
;   OTHER INFORMATION: Pro in position 36 is amidated
US-09-889-331A-189

  Query Match             62.9%;  Score 70.5;  DB 5;  Length 36;
  Best Local Similarity   59.4%;  Pred. No. 2.2e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 24, 2003, 23:06:00 ; Search time 72.5 Seconds
(without alignments)
141.898 Million cell updates/sec

Title: US-09-889-331A-48
Perfect score: 112
Sequence: 1 XXXGTXXXXXSKQXEEEAVRLXXXXLXGGXSSGAXXXXXX 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1171708 seqs, 257189365 residues

Total number of hits satisfying chosen parameters: 1171708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	79	70.5	40	5	US-09-889-331A-48	Sequence 48, Appl
2	70.5	62.9	36	1	PCT-US03-16699-171	Sequence 171, App
3	70.5	62.9	36	5	US-09-889-331A-189	Sequence 189, App
4	70.5	62.9	36	6	US-10-187-051-171	Sequence 171, App
5	70.5	62.9	36	6	US-10-157-224A-171	Sequence 171, App
6	70.5	62.9	36	6	US-10-342-014-171	Sequence 171, App
7	70.5	62.9	37	1	PCT-US03-16699-99	Sequence 99, Appl
8	70.5	62.9	37	1	PCT-US03-16699-183	Sequence 183, App
9	70.5	62.9	37	5	US-09-889-331A-109	Sequence 109, App
10	70.5	62.9	37	5	US-09-889-331A-201	Sequence 201, App
11	70.5	62.9	37	6	US-10-187-051-99	Sequence 99, Appl
12	70.5	62.9	37	6	US-10-187-051-183	Sequence 183, App
13	70.5	62.9	37	6	US-10-157-224A-99	Sequence 99, Appl
14	70.5	62.9	37	6	US-10-157-224A-183	Sequence 183, App
15	70.5	62.9	37	6	US-10-342-014-99	Sequence 99, Appl
16	70.5	62.9	37	6	US-10-342-014-183	Sequence 183, App
17	70.5	62.9	39	1	PCT-US03-16699-35	Sequence 35, Appl
18	70.5	62.9	39	1	PCT-US03-16699-36	Sequence 36, Appl
19	70.5	62.9	39	1	PCT-US03-16699-39	Sequence 39, Appl
20	70.5	62.9	39	5	US-09-889-331A-36	Sequence 36, Appl
21	70.5	62.9	39	5	US-09-889-331A-37	Sequence 37, Appl
22	70.5	62.9	39	5	US-09-889-331A-40	Sequence 40, Appl
23	70.5	62.9	39	6	US-10-187-051-35	Sequence 35, Appl
24	70.5	62.9	39	6	US-10-187-051-36	Sequence 36, Appl
25	70.5	62.9	39	6	US-10-187-051-39	Sequence 39, Appl
26	70.5	62.9	39	6	US-10-157-224A-35	Sequence 35, Appl
27	70.5	62.9	39	6	US-10-157-224A-36	Sequence 36, Appl
28	70.5	62.9	39	6	US-10-157-224A-39	Sequence 39, Appl
29	70.5	62.9	39	6	US-10-342-014-35	Sequence 35, Appl
30	70.5	62.9	39	6	US-10-342-014-36	Sequence 36, Appl
31	70.5	62.9	39	6	US-10-342-014-39	Sequence 39, Appl
32	69.5	62.1	35	1	PCT-US03-16699-69	Sequence 69, Appl
33	69.5	62.1	35	1	PCT-US03-16699-173	Sequence 173, App
34	69.5	62.1	35	5	US-09-889-331A-79	Sequence 79, Appl
35	69.5	62.1	35	5	US-09-889-331A-191	Sequence 191, App
36	69.5	62.1	35	6	US-10-187-051-69	Sequence 69, Appl
37	69.5	62.1	35	6	US-10-187-051-173	Sequence 173, App
38	69.5	62.1	35	6	US-10-157-224A-69	Sequence 69, Appl
39	69.5	62.1	35	6	US-10-157-224A-173	Sequence 173, App
40	69.5	62.1	35	6	US-10-342-014-69	Sequence 69, Appl
41	69.5	62.1	35	6	US-10-342-014-173	Sequence 173, App
42	69.5	62.1	36	1	PCT-US03-16699-67	Sequence 67, Appl
43	69.5	62.1	36	1	PCT-US03-16699-86	Sequence 86, Appl
44	69.5	62.1	36	1	PCT-US03-16699-170	Sequence 170, App
45	69.5	62.1	36	1	PCT-US03-16699-184	Sequence 184, App

ALIGNMENTS

```
RESULT 1
US-09-889-331A-48
; Sequence 48, Application US/09889331A
; GENERAL INFORMATION:
;  APPLICANT: YOUNG, ANDREW A.
;  APPLICANT:  GEDULIN, BRONISLAVA
;  TITLE OF INVENTION: METHODS FOR GLUCAGON SUPPRESSION
;  FILE REFERENCE: 030639.0031.UTL1 (249/167)
;  CURRENT APPLICATION NUMBER: US/09/889,331A
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: PCT/US00/00942
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 60/116,380
;  PRIOR FILING DATE: 1999-01-14
;  PRIOR APPLICATION NUMBER: 60/132,017
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: 60/175,365
;  PRIOR FILING DATE: 2000-01-10
;  NUMBER OF SEQ ID NOS: 239
;  SOFTWARE: FastSEQ for Windows Version 4.0
;    Microsoft WORD 97 SR-2
; SEQ ID NO 48
;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Construct
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)
;   OTHER INFORMATION: Xaa in position 1 is His, Arg, Tyr or
;   OTHER INFORMATION: 4-imidazopropionyl
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (2)
;   OTHER INFORMATION: Xaa in position 2 is Ser, Gly, Ala or Thr
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (3)
;   OTHER INFORMATION: Xaa in position 3 is Asp or Glu
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (6)
;   OTHER INFORMATION: Xaa in position 6 is Phe, Tyr or naphthylalanine
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (7)..(8)
;   OTHER INFORMATION: Xaa in positions 7 & 8 is Thr or Ser
```

Best Local Similarity 27.8%; Pred. No. 29;
Matches 10; Conservative 5; Mismatches 16; Indels 5; Gaps 1;

```
Qy          4 GTXXXXXSKQXEEEAVR-----LXXXXLXGGXSSGA 34
              |      ||:  |||::          : ||  :||
Db         78 GKKAAEESKEQIEEALKGADMVFVTAGMGGGTGTGA 113
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Search completed: June 24, 2003, 23:05:52
Job time : 14 secs

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DR   EMBL; M96425; AAA46903.1; -.
DR   PIR; A44062; A44062.
DR   MEROPS; C04.002; -.
DR   MEROPS; C06.001; -.
DR   MEROPS; S30.001; -.
DR   InterPro; IPR001410; DEAD.
DR   InterPro; IPR001650; Helicase_C.
DR   InterPro; IPR001730; Peptidase_C4.
DR   InterPro; IPR001456; Peptidase_C6.
DR   InterPro; IPR002540; Poty_P1.
DR   InterPro; IPR001592; Poty_coat.
DR   InterPro; IPR001205; RNA_pol_P3D.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00270; DEAD; 1.
DR   Pfam; PF00271; helicase_C; 1.
DR   Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR   Pfam; PF00767; Poty_coat; 1.
DR   Pfam; PF00851; Peptidase_C6; 1.
DR   Pfam; PF00863; Peptidase_C4; 1.
DR   Pfam; PF01577; Poty_P1; 1.
DR   PRINTS; PR00966; NIAPOTYPTASE.
DR   SMART; SM00487; DEXDc; 1.
DR   SMART; SM00490; HELICc; 1.
KW   Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
KW   Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;
KW   ATP-binding.
FT   CHAIN         1    287       N-TERMINAL PROTEIN.
FT   CHAIN       288    743       HELPER COMPONENT PROTEINASE.
FT   CHAIN       744      ?       PROTEIN P3.
FT   CHAIN         ?   1156       6 KDA PROTEIN 1.
FT   CHAIN      1157   1790       CYTOPLASMIC INCLUSION PROTEIN.
FT   CHAIN      1791   1842       6 KDA PROTEIN 2.
FT   CHAIN      1843      ?       GENOME-LINKED PROTEIN.
FT   CHAIN         ?   2276       NUCLEAR INCLUSION PROTEIN A.
FT   CHAIN      2277   2795       NUCLEAR INCLUSION PROTEIN B.
FT   CHAIN      2796   3068       COAT PROTEIN.
FT   BINDING    1906   1906       COVALENT LINKAGE OF VIRAL RNA
FT                                (BY SIMILARITY).
FT   NP_BIND    1241   1248       ATP (POTENTIAL).
SQ   SEQUENCE   3068 AA;  348651 MW;  FD3458B837FDA7C2 CRC64;

  Query Match           32.1%;  Score 36;  DB 1;  Length 3068;
  Best Local Similarity  80.0%;  Pred. No. 2.1e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRL 21
              || ||| |||
Db         87 KQREEEEVRL 96


RESULT 15
FTSZ_BACSU
ID   FTSZ_BACSU     STANDARD;      PRT;   382 AA.
AC   P17865;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Cell division protein ftsZ.
GN   FTSZ.
OS   Bacillus subtilis.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1423;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89008108; PubMed=3139638;
RA   Beall B., Lowe M., Lutkenhaus J.;
RT   "Cloning and characterization of Bacillus subtilis homologs of
RT   Escherichia coli cell division genes ftsZ and ftsA.";
RL   J. Bacteriol. 170:4855-4864(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RX   MEDLINE=98044033; PubMed=9384377;
RA   Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA   Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA   Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA   Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA   Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA   Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA   Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA   Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA   Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA   Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA   Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA   Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA   Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA   Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA   Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA   Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA   Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA   Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA   Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA   Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA   Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA   Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA   Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA   Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA   Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA   Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA   Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA   Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT   "The complete genome sequence of the Gram-positive bacterium Bacillus
RT   subtilis.";
RL   Nature 390:249-256(1997).
RN   [3]
RP   SEQUENCE OF 371-382 FROM N.A.
RX   MEDLINE=90216713; PubMed=2108961;
RA   Wu X.-C., Nathoo S., Pang A.S.-H., Carne T., Wang S.-L.;
RT   "Cloning, genetic organization, and characterization of a structural
RT   gene encoding bacillopeptidase F from Bacillus subtilis.";
RL   J. Biol. Chem. 265:6845-6850(1990).
CC   -!- FUNCTION: This protein is essential to the cell-division process.
CC       It seems to assemble into a dynamic ring on the inner surface of
CC       the cytoplasmic membrane at the place where division will occur,
CC       and the formation of the ring is the signal for septation to
CC       begin. Binds to and hydrolyzes GTP (By similarity).
CC   -!- SUBUNIT: Aggregates to form a ring-like structure (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic. Assembles at the inner surface
CC       of the cytoplasmic membrane (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE FTSZ FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M22630; AAA22457.1; -.
DR   EMBL; Z99111; CAB13402.1; -.
DR   EMBL; J05400; AAA83361.1; -.
DR   HSSP; Q57816; 1FSZ.
DR   SubtiList; BG10232; ftsZ.
DR   InterPro; IPR000158; FtsZ.
DR   InterPro; IPR003008; Tubulin_FtsZ.
DR   Pfam; PF00091; tubulin; 1.
DR   PRINTS; PR00423; CELLDVISFTSZ.
DR   TIGRFAMs; TIGR00065; ftsZ; 1.
DR   PROSITE; PS01134; FTSZ_1; 1.
DR   PROSITE; PS01135; FTSZ_2; 1.
KW   Cell division; Septation; GTP-binding; Complete proteome.
FT   NP_BIND     104    112       GTP (POTENTIAL).
SQ   SEQUENCE   382 AA;  40355 MW;  D1E908DED2734CBE CRC64;

  Query Match           31.7%;  Score 35.5;  DB 1;  Length 382;
```

```
Qy          11 SKQXEEEAVRLXXXXLXGGXSSGA 34
               :|: ||   :|    : || ::|:
Db         765 NKRAEEAERKLVEMKMQGGAATGS 788


RESULT 13
CARB_SULTO
ID   CARB_SULTO     STANDARD;      PRT;  1049 AA.
AC   Q970U7;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-
DE   phosphate synthetase ammonia chain).
GN   CARB OR ST1504.
OS   Sulfolobus tokodaii.
OC   Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC   Sulfolobus.
OX   NCBI_TaxID=111955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=JCM 10545 / 7;
RX   MEDLINE=21456156; PubMed=11572479;
RA   Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA   Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA   Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA   Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA   Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA   Oshima T., Kikuchi H.;
RT   "Complete genome sequence of an aerobic thermoacidophilic
RT   Crenarchaeon, Sulfolobus tokodaii strain7.";
RL   DNA Res. 8:123-140(2001).
CC   -!- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP +
CC       phosphate + L-glutamate + carbamoyl phosphate.
CC   -!- COFACTOR: Binds three manganese ions (By similarity).
CC   -!- PATHWAY: Arginine biosynthesis;
CC   -!- PATHWAY: Pyrimidine biosynthesis; first step.
CC   -!- SUBUNIT: Composed of two chains; the small (or glutamine) chain
CC       promotes the hydrolysis of glutamine to ammonia, which is used by
CC       the large (or ammonia) chain to synthesize carbamoyl phosphate (By
CC       similarity).
CC   -!- SIMILARITY: BELONGS TO THE CARB FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AP000986; BAB66576.1; -.
DR   InterPro; IPR005479; CPase_L_D2.
DR   InterPro; IPR005480; CPase_L_D3.
DR   InterPro; IPR005481; CPase_L_N.
DR   Pfam; PF00289; CPSase_L_chain; 2.
DR   Pfam; PF02786; CPSase_L_D2; 2.
DR   Pfam; PF02787; CPSase_L_D3; 1.
DR   PROSITE; PS00866; CPSASE_1; 1.
DR   PROSITE; PS00867; CPSASE_2; 1.
KW   Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
KW   ATP-binding; Manganese; Complete proteome.
FT   DOMAIN        1    399       CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
FT   DOMAIN      400    548       OLIGOMERIZATION DOMAIN.
FT   DOMAIN      549    930       CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
FT   DOMAIN      931   1049       ALLOSTERIC DOMAIN.
FT   REPEAT        1    548
FT   REPEAT      549   1049
FT   NP_BIND     151    208       ATP (POTENTIAL).
FT   NP_BIND     300    350       ATP (POTENTIAL).
FT   METAL       282    282       MANGANESE 1 (BY SIMILARITY).
FT   METAL       296    296       MANGANESE 1 AND 2 (BY SIMILARITY).
FT   METAL       298    298       MANGANESE 2 (BY SIMILARITY).
FT   METAL       823    823       MANGANESE 3 (BY SIMILARITY).
FT   METAL       835    835       MANGANESE 3 (BY SIMILARITY).
SQ   SEQUENCE   1049 AA;  117504 MW;  41FB6EFE1A1F94AF CRC64;

  Query Match           32.1%;  Score 36;  DB 1;  Length 1049;
  Best Local Similarity  63.6%;  Pred. No. 68;
  Matches    7;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          11 SKQXEEEAVRL 21
               ||: ||| :||
Db         646 SKKLEEEGIRL 656


RESULT 14
POLG_PEMVC
ID   POLG_PEMVC     STANDARD;      PRT;  3068 AA.
AC   Q01500;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Genome polyprotein [Contains: N-terminal protein (P1); Helper
DE   component proteinase (EC 3.4.22.45) (HC-Pro); Protein P3; 6 kDa
DE   protein 1 (6K1); Cytoplasmic inclusion protein (CI); 6 kDa protein 2
DE   (6K2); Genome-linked protein (VPG); Nuclear inclusion protein A (NI-A)
DE   (NIA) (EC 3.4.22.44) (49 kDa proteinase) (49 kDa-Pro); Nuclear
DE   inclusion protein B (NI-B) (NIB) (RNA-directed RNA polymerase) (EC
DE   2.7.7.48); Coat protein (CP)].
OS   Pepper mottle virus (California isolate) (PeMV) (PepMoV C).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC   Potyvirus.
OX   NCBI_TaxID=31737;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93033110; PubMed=1413501;
RA   Vance V.B., Moore D., Turpen T.H., Bracker A., Hollowell V.C.;
RT   "The complete nucleotide sequence of pepper mottle virus genomic RNA:
RT   comparison of the encoded polyprotein with those of other sequenced
RT   potyviruses.";
RL   Virology 191:19-30(1992).
CC   -!- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID
CC       TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
CC   -!- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
CC       MAY BE INVOLVED IN REPLICATION.
CC   -!- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
CC   -!- CATALYTIC ACTIVITY: Hydrolyzes glutaminyl bonds, and activity is
CC       further restricted by preferences for the amino acids in P6 - P1'
CC       that vary with the species of potyvirus, e.g. Glu-Xaa-Xaa-Tyr-Xaa-
CC       Gln+(Ser or Gly) for the enzyme from tobacco etch virus. The
CC       natural substrate is the viral polyprotein, but other proteins and
CC       oligopeptides containing the appropriate consensus sequence are
CC       also cleaved.
CC   -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC       {RNA}(N).
CC   -!- CATALYTIC ACTIVITY: Hydrolyzes a Gly-|-Gly bond at its own C-
CC       terminus, commonly in the sequence -Tyr-Xaa-Val-Gly-|-Gly, in the
CC       processing of the potyviral polyprotein.
CC   -!- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
CC   -!- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
CC       POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
CC       PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
CC       INDIVIDUAL PROTEINS.
CC   -!- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
CC   -!- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
CC   -!- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
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  Query Match             32.1%;  Score 36;  DB 1;  Length 344;
  Best Local Similarity   30.4%;  Pred. No. 21;
  Matches    7;  Conservative    3;  Mismatches   13;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLXGGXSSGA 34
              :|  |: : |    |  |   ||
Db        261 EQSHEDGITLTSTTLVNGAVEGA 283


RESULT 11
SP4_HUMAN
ID   SP4_HUMAN      STANDARD;      PRT;   784 AA.
AC   Q02446; O60402;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Transcription factor Sp4 (SPR-1).
GN   SP4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Uterus;
RX   MEDLINE=93087156; PubMed=1454515;
RA   Hagen G., Mueller S., Beato M., Suske G.;
RT   "Cloning by recognition site screening of two novel GT box binding
RT   proteins: a family of Sp1 related genes.";
RL   Nucleic Acids Res. 20:5519-5525(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Ozersky P., Holmes A.;
RL   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: BINDS TO GT AND GC BOXES PROMOTERS ELEMENTS. PROBABLE
CC       TRANSCRIPTIONAL ACTIVATOR.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- TISSUE SPECIFICITY: ABUNDANT IN BRAIN.
CC   -!- SIMILARITY: BELONGS TO THE SP1 FAMILY OF C2H2-TYPE ZINC-FINGER
CC       PROTEINS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X68561; CAA48563.1; -.
DR   EMBL; AC004595; AAD12226.1; -.
DR   PIR; S26638; S26638.
DR   HSSP; P08047; 1SP1.
DR   TRANSFAC; T02339; -.
DR   Genew; HGNC:11209; SP4.
DR   MIM; 600540; -.
DR   InterPro; IPR000822; Znf_C2H2.
DR   Pfam; PF00096; zf-C2H2; 3.
DR   PRINTS; PR00048; ZINCFINGER.
DR   ProDom; PD000003; Znf_C2H2; 2.
DR   SMART; SM00355; ZnF_C2H2; 3.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
KW   Transcription regulation; Activator; Zinc-finger; Metal-binding;
KW   DNA-binding; Nuclear protein; Repeat.
FT   DOMAIN        7     11       POLY-GLU.
FT   DOMAIN       12     19       POLY-ALA.
FT   DOMAIN      122    130       POLY-SER.
FT   DOMAIN      185    188       POLY-SER.
FT   DOMAIN      647    729       ZINC FINGERS.
FT   ZN_FING     647    671       C2H2-TYPE.
FT   ZN_FING     677    701       C2H2-TYPE.
FT   ZN_FING     707    729       C2H2-TYPE.
FT   CONFLICT    197    197       K -> Q (IN REF. 2).
FT   CONFLICT    379    380       HA -> QP (IN REF. 2).
FT   CONFLICT    386    386       Q -> A (IN REF. 2).
SQ   SEQUENCE   784 AA;  82025 MW;  3C4EAE28CB2B81FB CRC64;

  Query Match             32.1%;  Score 36;  DB 1;  Length 784;
  Best Local Similarity   38.1%;  Pred. No. 50;
  Matches    8;  Conservative    2;  Mismatches   11;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLXGGXSS 32
              |: ||||         || :|
Db          6 KEEEEEAAAAAAMATEGGKTS 26


RESULT 12
NUC1_NEUCR
ID   NUC1_NEUCR     STANDARD;      PRT;   823 AA.
AC   P20824;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Phosphorus acquisition controlling protein.
GN   NUC-1.
OS   Neurospora crassa.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariales; Sordariaceae; Neurospora.
OX   NCBI_TaxID=5141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=40-21;
RX   MEDLINE=91042513; PubMed=2146493;
RA   Kang S., Metzenberg R.L.;
RT   "Molecular analysis of nuc-1+, a gene controlling phosphorus
RT   acquisition in Neurospora crassa.";
RL   Mol. Cell. Biol. 10:5839-5848(1990).
CC   -!- FUNCTION: FACTOR THAT ACTIVATES THE TRANSCRIPTION OF STRUCTURAL
CC       GENES FOR PHOSPHORUS ACQUISITION.
CC   -!- SUBUNIT: BINDS DNA AS A DIMER.
CC   -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC       TRANSCRIPTION FACTORS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M37700; AAA33603.1; -.
DR   PIR; A36378; A36378.
DR   HSSP; P07270; 1A0A.
DR   TRANSFAC; T01642; -.
DR   InterPro; IPR001092; HLH_basic.
DR   Pfam; PF00010; HLH; 1.
DR   SMART; SM00353; HLH; 1.
DR   PROSITE; PS00038; HLH_1; 1.
DR   PROSITE; PS50888; HLH_2; 1.
KW   DNA-binding; Transcription regulation; Nuclear protein; Activator.
FT   DOMAIN       22     51       ASP-RICH (ACIDIC).
FT   DOMAIN      101    220       GLN-RICH (INVOLVED IN TRANSCRIPTIONAL
FT                                ACTIVATION) (POTENTIAL).
FT   DOMAIN      434    556       PRO-RICH.
FT   DOMAIN      468    562       INTERACTION WITH NEGATIVE REGULATORY
FT                                FACTOR (POTENTIAL).
FT   DOMAIN      718    758       HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
SQ   SEQUENCE   823 AA;  87275 MW;  5E513ED989666E2F CRC64;

  Query Match             32.1%;  Score 36;  DB 1;  Length 823;
  Best Local Similarity   29.2%;  Pred. No. 53;
  Matches    7;  Conservative    7;  Mismatches   10;  Indels    0;  Gaps    0;
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FT   DISULFID    208    256       BY SIMILARITY.
FT   DISULFID    468    468       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD     81     81       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    288    288       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    389    389       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     168    168       H -> N (IN STRAIN 129/SV).
FT   CONFLICT     58     59       DS -> IT (IN REF. 1).
FT   CONFLICT    132    132       E -> G (IN REF. 1).
FT   CONFLICT    293    293       G -> V (IN REF. 3).
FT   CONFLICT    348    348       Y -> C (IN REF. 3).
SQ   SEQUENCE   536 AA;  59841 MW;  22E14B5C454F4427 CRC64;

  Query Match             33.0%;  Score 37;  DB 1;  Length 536;
  Best Local Similarity   56.2%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         19 VRLXXXXLXGGXSSGA 34
              | |    | || ||||
Db         13 VLLARVLLAGGASSGA 28


RESULT 9
C561_HUMAN
ID   C561_HUMAN     STANDARD;      PRT;   251 AA.
AC   P49447;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Cytochrome b561 (Cytochrome b-561).
GN   CYB561.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood;
RX   MEDLINE=96032691; PubMed=7559396;
RA   Srivastava M.;
RT   "Genomic structure and expression of the human gene encoding
RT   cytochrome b561, an integral protein of the chromaffin granule
RT   membrane.";
RL   J. Biol. Chem. 270:22714-22720(1995).
RN   [2]
RP   SEQUENCE OF 6-251 FROM N.A.
RC   TISSUE=Caudate;
RX   MEDLINE=95071309; PubMed=7980462;
RA   Srivastava M., Gibson K.R., Pollard H.B., Fleming P.J.;
RT   "Human cytochrome b561: a revised hypothesis for conformation in
RT   membranes which reconciles sequence and functional information.";
RL   Biochem. J. 303:915-921(1994).
CC   -!- FUNCTION: SECRETORY VESICLE-SPECIFIC ELECTRON TRANSPORT PROTEIN.
CC   -!- COFACTOR: BINDS TWO HEME GROUPS NON-COVALENTLY (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE EUKARYOTIC B561 FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U29462; AAC50212.1; -.
DR   EMBL; U29460; AAC50212.1; JOINED.
DR   EMBL; U29461; AAC50212.1; JOINED.
DR   EMBL; U29464; AAC50212.1; JOINED.
DR   EMBL; U29469; AAC50212.1; JOINED.
DR   EMBL; U06715; AAA50952.1; -.
DR   Genew; HGNC:2571; CYB561.
DR   MIM; 600019; -.
DR   InterPro; IPR004877; Cyt_B561.
DR   Pfam; PF03188; Cytochrome_B561; 1.
KW   Electron transport; Transmembrane; Heme.
FT   DOMAIN        1     15       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     16     38       POTENTIAL.
FT   TRANSMEM     53     75       POTENTIAL.
FT   TRANSMEM     85    107       POTENTIAL.
FT   TRANSMEM    123    145       POTENTIAL.
FT   TRANSMEM    163    185       POTENTIAL.
FT   TRANSMEM    197    219       POTENTIAL.
FT   DOMAIN      220    251       CYTOPLASMIC (POTENTIAL).
FT   METAL        53     53       IRON (HEME) (POTENTIAL).
FT   METAL        87     87       IRON (HEME) (POTENTIAL).
FT   METAL        91     91       IRON (HEME) (POTENTIAL).
FT   METAL       109    109       IRON (HEME) (POTENTIAL).
FT   METAL       121    121       IRON (HEME) (POTENTIAL).
FT   METAL       160    160       IRON (HEME) (POTENTIAL).
SQ   SEQUENCE   251 AA;  27623 MW;  3F14C776BDAB0B6A CRC64;

  Query Match             32.1%;  Score 36;  DB 1;  Length 251;
  Best Local Similarity   36.4%;  Pred. No. 15;
  Matches    8;  Conservative    4;  Mismatches   10;  Indels    0;  Gaps    0;

Qy         13 QXEEEAVRLXXXXLXGGXSSGA 34
              | ||:|: :    |  | | |:
Db        229 QAEEQALSMDFKTLRQGDSPGS 250


RESULT 10
VU79_HSV6U
ID   VU79_HSV6U     STANDARD;      PRT;   344 AA.
AC   P52529;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Protein U79.
GN   U79 OR EDRF1.
OS   Human herpesvirus (type 6 / strain Uganda-1102) (HHV6).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Betaherpesvirinae; Roseolovirus.
OX   NCBI_TaxID=10370;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95027704; PubMed=7941342;
RA   Nicholas J.;
RT   "Nucleotide sequence analysis of a 21-kbp region of the genome of
RT   human herpesvirus-6 containing homologues of human cytomegalovirus
RT   major immediate-early and replication genes.";
RL   Virology 204:738-750(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95266321; PubMed=7747482;
RA   Gompels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,
RA   Martin M.E., Efstathiou S., Craxton M., Macaulay H.A.;
RT   "The DNA sequence of human herpesvirus-6: structure, coding content,
RT   and genome evolution.";
RL   Virology 209:29-51(1995).
CC   -!- FUNCTION: POSSIBLE REPLICATION PROTEIN.
CC   -!- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER HSV-6 AND
CC       HSV-7 U79 AND HCMV UL112 (P34).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U13194; AAA68470.1; -.
DR   EMBL; X83413; CAA58371.1; -.
DR   InterPro; IPR004138; U79_P34.
DR   Pfam; PF03064; U79_P34; 1.
SQ   SEQUENCE   344 AA;  39272 MW;  E34F1FE7ADB7D790 CRC64;
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CC       positive bacteria B.cereus, B.subtilis, S.pyrogenes, M.fortuitum,
CC       S.aureus and L.monocytogenes and against Gram-negative bacteria
CC       E.coli, E.cloacae, S.typhimurium, K.pneumoniae and P.auruginosa.
CC       Possesses antifungal activity against N.crassa, A.fumigatus,
CC       A.brassicola, N.hematococca, F.culmorum and F.oxyporum and
CC       against S.cereviase and C.albicans yeast. Inactive against
CC       T.mentagrophytes.
CC   -!- SUBCELLULAR LOCATION: Neuroendocrine and endocrine secretory
CC       granules.
CC   -!- MASS SPECTROMETRY: MW=8584.9; METHOD=MALDI; RANGE=19-94.
CC   -!- MISCELLANEOUS: Binds calcium with a low-affinity.
CC   -!- SIMILARITY: BELONGS TO THE CHROMOGRANIN / SECRETOGRANIN PROTEIN
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; S79270; AAB21297.1; -.
DR   EMBL; S79256; AAB21297.1; JOINED.
DR   EMBL; S79258; AAB21297.1; JOINED.
DR   EMBL; S79260; AAB21297.1; JOINED.
DR   EMBL; S79262; AAB21297.1; JOINED.
DR   EMBL; S79264; AAB21297.1; JOINED.
DR   EMBL; S79266; AAB21297.1; JOINED.
DR   EMBL; S79268; AAB21297.1; JOINED.
DR   EMBL; X04012; CAA27636.1; -.
DR   EMBL; X04298; CAA27841.1; -.
DR   EMBL; M16971; AAA30765.1; -.
DR   EMBL; U73523; AAC48700.1; -.
DR   PIR; A41520; A41520.
DR   PIR; A24175; A24175.
DR   PIR; A28033; A28033.
DR   PDB; 1CFK; 22-MAR-99.
DR   GlycoSuiteDB; P05059; -.
DR   InterPro; IPR001819; Chromogranin_AB.
DR   InterPro; IPR001990; Granin.
DR   Pfam; PF01271; Granin; 1.
DR   PRINTS; PR00659; CHROMOGRANIN.
DR   PROSITE; PS00422; GRANINS_1; 1.
DR   PROSITE; PS00423; GRANINS_2; 1.
KW   Signal; Amidation; Glycoprotein; Calcium-binding; Phosphorylation;
KW   Polymorphism; 3D-structure; Antibiotic; Fungicide.
FT   SIGNAL       1     18
FT   CHAIN       19    449       CHROMOGRANIN A.
FT   PEPTIDE     19     94       VASOSTATIN-1.
FT   PEPTIDE    142    161       CHROMOSTATIN.
FT   PEPTIDE    191    212       CHROMACIN.
FT   PEPTIDE    266    312       PANCREASTATIN.
FT   PEPTIDE    334    347       WE-14.
FT   PEPTIDE    362    382       CATESTATIN.
FT   MOD_RES     99     99       PHOSPHORYLATION (PARTIAL).
FT   MOD_RES    142    142       PHOSPHORYLATION (PARTIAL).
FT   MOD_RES    191    191       PHOSPHORYLATION.
FT   MOD_RES    315    315       PHOSPHORYLATION (PARTIAL).

  Query Match             33.0%;  Score 37;  DB 1;  Length 449;
  Best Local Similarity   42.9%;  Pred. No. 18;
  Matches    9;  Conservative    1;  Mismatches   11;  Indels    0;  Gaps    0;

Qy         11 SKQXEEEAVRLXXXXLXGGXS 31
              |:| |||  |       || |
Db        295 SRQEEEEMARAPQVLFRGGKS 315


RESULT 8
ANPC_MOUSE
ID   ANPC_MOUSE     STANDARD;      PRT;   536 AA.
AC   P70180; P97804; Q9R025; Q9R028;
DT   15-JUL-1998 (Rel. 36, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Atrial natriuretic peptide clearance receptor precursor (ANP-C)
DE   (ANPRC) (NPR-C) (Atrial natriuretic peptide C-type receptor) (EF-2).
GN   NPR3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Lung;
RX   MEDLINE=96203905; PubMed=8620881;
RA   Yanaka N., Kotera J., Taguchi I., Sugiura M., Kawashima K., Omori K.;
RT   "Structure of the 5'-flanking regulatory region of the mouse gene
RT   encoding the clearance receptor for atrial natriuretic peptide.";
RL   Eur. J. Biochem. 237:25-34(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c, and 129/Sv;
RX   MEDLINE=99398699; PubMed=10468599;
RA   Jaubert J., Jaubert F., Martin N., Washburn L.L., Lee B.K.,
RA   Eicher E.M., Guenet J.-L.;
RT   "Three new allelic mouse mutations that cause skeletal overgrowth
RT   involve the natriuretic peptide receptor C gene (Npr3).";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:10278-10283(1999).
RN   [3]
RP   SEQUENCE OF 255-439 FROM N.A.
RX   MEDLINE=97184476; PubMed=9032278;
RA   Fu X., Kamps M.P.;
RT   "E2a-Pbx1 induces aberrant expression of tissue-specific and
RT   developmentally regulated genes when expressed in NIH 3T3
RT   fibroblasts.";
RL   Mol. Cell. Biol. 17:1503-1512(1997).
CC   -!- FUNCTION: RECEPTOR FOR ATRIAL NATRIURETIC PEPTIDE. DOES NOT HAVE
CC       GUANYLATE CYCLASE ACTIVITY.
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE ANP RECEPTORS: TWO
CC       WITH GUANYLATE CYCLASE ACTIVITY (ANP-A AND ANP-B) AND ONE (ANP-C)
CC       WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF ANP FROM THE
CC       CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.
CC   -!- SIMILARITY: TO ANP-A AND ANP-B RECEPTOR IN THEIR EXTRACELLULAR AND
CC       TRANSMEMBRANE DOMAINS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D78175; BAA11241.1; -.
DR   EMBL; AF131861; AAF00104.1; -.
DR   EMBL; AF131864; AAF00107.1; -.
DR   EMBL; U72676; AAB51036.1; -.
DR   MGD; MGI:97373; Npr3.
DR   InterPro; IPR001828; ANF_receptor.
DR   InterPro; IPR001170; Ntpep_receptorN.
DR   Pfam; PF01094; ANF_receptor; 1.
DR   PRINTS; PR00255; NATPEPTIDER.
DR   PROSITE; PS00458; ANF_RECEPTORS; 1.
KW   Receptor; Glycoprotein; Transmembrane; Signal.
FT   SIGNAL       1     26       POTENTIAL.
FT   PROPEP      27     40       POTENTIAL.
FT   CHAIN       41    536       ATRIAL NATRIURETIC PEPTIDE CLEARANCE
FT                               RECEPTOR.
FT   DOMAIN      41    478       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   479    499       POTENTIAL.
FT   DOMAIN     500    536       CYTOPLASMIC (POTENTIAL).
FT   DISULFID   103    131       BY SIMILARITY.
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Db         28 EQTPEEAVEIARAAIRGG 45


RESULT 7
CMGA_BOVIN
ID   CMGA_BOVIN     STANDARD;      PRT;   449 AA.
AC   P05059; P79392;
DT   13-AUG-1987 (Rel. 05, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Chromogranin A precursor (CGA) (Pituitary secretory protein I) (SP-I)
DE   [Contains: Vasostatin-1; Chromostatin; Chromacin; Pancreastatin; WE-
DE   14; Catestatin].
GN   CHGA.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92140395; PubMed=1779968;
RA   Iacangelo A.L., Grimes M., Eiden L.E.;
RT   "The bovine chromogranin A gene: structural basis for hormone
RT   regulation and generation of biologically active peptides.";
RL   Mol. Endocrinol. 5:1651-1660(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86300648; PubMed=3755681;
RA   Benedum U.M., Baeuerle P.A., Konecki D.S., Frank R., Powell J.,
RA   Mallet J., Huttner W.B.;
RT   "The primary structure of bovine chromogranin A: a representative of
RT   a class of acidic secretory proteins common to a variety of
RT   peptidergic cells.";
RL   EMBO J. 5:1495-1502(1986).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86311345; PubMed=3018587;
RA   Iacangelo A., Affolter H.-U., Eiden L.E., Herbert E., Grimes M.;
RT   "Bovine chromogranin A sequence and distribution of its messenger RNA
RT   in endocrine tissues.";
RL   Nature 323:82-86(1986).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87260925; PubMed=3474638;
RA   Ahn T.G., Cohn D.V., Gorr S.U., Ornstein D.L., Kashdan M.A.,
RA   Levine M.A.;
RT   "Primary structure of bovine pituitary secretory protein I
RT   (chromogranin A) deduced from the cDNA sequence.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:5043-5047(1987).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97228583; PubMed=9074643;
RA   Kang Y.K., Yoo S.H.;
RT   "Identification of the secretory vesicle membrane binding region of
RT   chromogranin A.";
RL   FEBS Lett. 404:87-90(1997).
RN   [6]
RP   SEQUENCE OF 19-45, AND CALCIUM-BINDING.
RX   MEDLINE=90354431; PubMed=2387861;
RA   Yoo S.H., Albanesi J.P.;
RT   "Ca2(+)-induced conformational change and aggregation of chromogranin
RT   A.";
RL   J. Biol. Chem. 265:14414-14421(1990).
RN   [7]
RP   SEQUENCE OF 142-161, AND SYNTHESIS OF CHROMOSTATIN.
RX   MEDLINE=91142185; PubMed=1996343;
RA   Galindo E., Rill A., Bader M.-F., Aunis D.;
RT   "Chromostatin, a 20-amino acid peptide derived from chromogranin A,
RT   inhibits chromaffin cell secretion.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:1426-1430(1991).
RN   [8]
RP   ERRATUM.
RA   Galindo E., Rill A., Bader M.-F., Aunis D.;
RL   Proc. Natl. Acad. Sci. U.S.A. 91:832-832(1994).
RN   [9]
RP   SEQUENCE OF 266-312.
RX   MEDLINE=89331945; PubMed=2756155;
RA   Nakano I., Funakoshi A., Miyasaka K., Ishida K., Makk G., Angwin P.,
RA   Chang D., Tatemoto K.;
RT   "Isolation and characterization of bovine pancreastatin.";
RL   Regul. Pept. 25:207-213(1989).
RN   [10]
RP   SEQUENCE OF 191-212 (CHROMACIN), PHOSPHORYLATION SITE SER-191, AND
RP   O-GLYCOSYLATION OF SER-204.
RC   TISSUE=Chromaffin granules;
RX   MEDLINE=97067080; PubMed=8910482;
RA   Strub J.-M., Goumon Y., Lugardon K., Capon C., Lopez M., Moniatte M.,
RA   van Dorsselaer A., Aunis D., Metz-Boutigue M.-H.;
RT   "Antibacterial activity of glycosylated and phosphorylated
RT   chromogranin A-derived peptide 173-194 from bovine adrenal medullary
RT   chromaffin granules.";
RL   J. Biol. Chem. 271:28533-28540(1996).
RN   [11]
RP   CHARACTERIZATION OF CATESTATIN.
RX   MEDLINE=97439785; PubMed=9294131;
RA   Mahata S.K., O'Connor D.T., Mahata M., Yoo S.H., Taupenot L., Wu H.,
RA   Gill B.M., Parmer R.J.;
RT   "Novel autocrine feedback control of catecholamine release. A discrete
RT   chromogranin a fragment is a noncompetitive nicotinic cholinergic
RT   antagonist.";
RL   J. Clin. Invest. 100:1623-1633(1997).
RN   [12]
RP   CHARACTERIZATION OF CATESTATIN.
RX   MEDLINE=99000113; PubMed=9786174;
RA   Kennedy B.P., Mahata S.K., O'Connor D.T., Ziegler M.G.;
RT   "Mechanism of cardiovascular actions of the chromogranin A fragment
RT   catestatin in vivo.";
RL   Peptides 19:1241-1248(1998).
RN   [13]
RP   3D-STRUCTURE MODELING OF CATESTATIN.
RX   MEDLINE=99025667; PubMed=9809795;
RA   Tsigelny I., Mahata S.K., Taupenot L., Preece N.E., Mahata M.,
RA   Khan I., Parmer R.J., O'Connor D.T.;
RT   "Mechanism of action of chromogranin A on catecholamine release:
RT   molecular modeling of the catestatin region reveals a beta-
RT   strand/loop/beta-strand structure secured by hydrophobic interactions
RT   and predictive of activity.";
RL   Regul. Pept. 77:43-53(1998).
RN   [14]
RP   CHARACTERIZATION OF VASOSTATIN-1.
RX   MEDLINE=20219105; PubMed=10753865;
RA   Lugardon K., Raffner R., Goumon Y., Corti A., Delmas A., Bulet P.,
RA   Aunis D., Metz-Boutigue M.-H.;
RT   "Antibacterial and antifungal activities of vasostatin-1, the N-
RT   terminal fragment of chromogranin A.";
RL   J. Biol. Chem. 275:10745-10753(2000).
RN   [15]
RP   CARBOHYDRATE-LINKAGE SITES, PHOSPHORYLATION, AND DISULFIDE BOND.
RX   MEDLINE=99459228; PubMed=10527498;
RA   Bauer S.H., Zhang X.Y., Van Dongen W., Claeys M., Przybylski M.;
RT   "Chromogranin A from bovine adrenal medulla: molecular
RT   characterization of glycosylations, phosphorylations, and sequence
RT   heterogeneities by mass spectrometry.";
RL   Anal. Biochem. 274:69-80(1999).
CC   -!- FUNCTION: Pancreastatin strongly inhibits glucose induced insulin
CC       release from the pancreas.
CC   -!- FUNCTION: Chromostatin completely inhibits catecholamine release
CC       from chromaffin cells.
CC   -!- FUNCTION: Chromacin has antibacterial activity against M.luteus.
CC       Not active against E.coli.
CC   -!- FUNCTION: Catestatin inhibits catecholamine release from
CC       chromaffin cells and noradrenergic neurons by acting as a non-
CC       competitive nicotinic cholinergic antagonist.
CC   -!- FUNCTION: Vasostatin-1 has antibacterial activity against Gram-
CC       positive bacteria M.luteus, B.megaterium. Not active against Gram-
```

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RA   Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA   Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
RA   Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S.,
RA   Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA   Yamagata S., Horiuchi T.;
RT   "Construction of a contiguous 874-kb sequence of the Escherichia coli
RT   - K12 genome corresponding to 50.0-68.8 min on the linkage map and
RT   analysis of its sequence features.";
RL   DNA Res. 4:91-113(1997).
RN   [4]
RP   IDENTIFICATION.
RA   Rudd K.E.;
RL   Unpublished observations (AUG-1994).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE000323; AAC75407.1; -.
DR   EMBL; D90865; BAA16207.1; -.
DR   EMBL; U11296; -; NOT_ANNOTATED_CDS.
DR   EcoGene; EG12420; yfdC.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   310 AA;  34503 MW;  96D34F450B209ED3 CRC64;

  Query Match             33.9%;  Score 38;  DB 1;  Length 310;
  Best Local Similarity   34.8%;  Pred. No. 7.9;
  Matches    8;  Conservative    4;  Mismatches   11;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLXGGXSSGA 34
              |: | :|: |    :  | | ||
Db         50 KELERDAMALLWSAIAAGLSMGA 72


RESULT 5
Y4WA_RHISN
ID   Y4WA_RHISN     STANDARD;      PRT;   512 AA.
AC   P55679;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Hypothetical zinc protease y4wA (EC 3.4.99.-).
GN   Y4WA.
OS   Rhizobium sp. (strain NGR234).
OG   Plasmid sym pNGR234a.
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Rhizobiaceae; Rhizobium.
OX   NCBI_TaxID=394;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97305956; PubMed=9163424;
RA   Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA   Perret X.;
RT   "Molecular basis of symbiosis between Rhizobium and Legumes.";
RL   Nature 387:394-401(1997).
CC   -!- COFACTOR: REQUIRES DIVALENT CATIONS FOR ACTIVITY. BINDS ZINC (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M16.
CC   -!- SIMILARITY: TO Y4WB.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE000103; AAB91908.1; -.
DR   MEROPS; M16.UPB; -.
DR   InterPro; IPR001431; Peptidase_M16.
DR   Pfam; PF00675; Peptidase_M16; 1.
DR   PROSITE; PS00143; INSULINASE; 1.
KW   Hypothetical protein; Hydrolase; Metalloprotease; Zinc;
KW   Transmembrane; Plasmid.
FT   TRANSMEM     57     77       POTENTIAL.
FT   METAL       131    131       ZINC (BY SIMILARITY).
FT   ACT_SITE    134    134       BY SIMILARITY.
FT   METAL       135    135       ZINC (BY SIMILARITY).
FT   METAL       211    211       ZINC (BY SIMILARITY).
SQ   SEQUENCE   512 AA;  56886 MW;  7BDC60C11F08BD85 CRC64;

  Query Match             33.9%;  Score 38;  DB 1;  Length 512;
  Best Local Similarity   32.1%;  Pred. No. 13;
  Matches    9;  Conservative    4;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          5 TXXXXXSKQXEEEAVRLXXXXLXGGXSS 32
              |     ::| | ||: :    | ||  |
Db        335 TTSYGTAEQGEAEALDILSEILGGGTRS 362


RESULT 6
PCRB_METTH
ID   PCRB_METTH     STANDARD;      PRT;   248 AA.
AC   O26652;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   PcrB protein homolog.
GN   PCRB OR MTH552.
OS   Methanobacterium thermoautotrophicum.
OC   Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC   Methanobacteriaceae; Methanothermobacter.
OX   NCBI_TaxID=187420;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Delta H;
RX   MEDLINE=98037514; PubMed=9371463;
RA   Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA   Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA   Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA   Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA   Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA   McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA   Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT   "Complete genome sequence of Methanobacterium thermoautotrophicum
RT   deltaH: functional analysis and comparative genomics.";
RL   J. Bacteriol. 179:7135-7155(1997).
CC   -!- SIMILARITY: BELONGS TO THE PCRB FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE000838; AAB85058.1; -.
DR   InterPro; IPR003009; FMN_enzyme.
DR   InterPro; IPR002911; PcrB.
DR   Pfam; PF01884; PcrB; 1.
DR   TIGRFAMs; TIGR00265; PcrB; 1.
KW   Complete proteome.
SQ   SEQUENCE   248 AA;  26525 MW;  F59DAE240731E662 CRC64;

  Query Match             33.0%;  Score 37;  DB 1;  Length 248;
  Best Local Similarity   38.9%;  Pred. No. 9.7;
  Matches    7;  Conservative    3;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLXGG 29
              :|  |||| :    : ||
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```
OC   Heloderma.
OX   NCBI_TaxID=8554;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97172477; PubMed=9020121;
RA   Chen Y.E., Drucker D.J.;
RT   "Tissue-specific expression of unique mRNAs that encode proglucagon-
RT   derived peptides or exendin 4 in the lizard.";
RL   J. Biol. Chem. 272:4108-4115(1997).
RN   [2]
RP   SEQUENCE OF 48-86.
RC   TISSUE=Venom;
RX   MEDLINE=92218391; PubMed=1313797;
RA   Eng J., Kleinman W.A., Singh L., Singh G., Raufman J.-P.;
RT   "Isolation and characterization of exendin-4, an exendin-3 analogue,
RT   from Heloderma suspectum venom. Further evidence for an exendin
RT   receptor on dispersed acini from guinea pig pancreas.";
RL   J. Biol. Chem. 267:7402-7405(1992).
CC   -!- FUNCTION: HAS A VIP/SECRETIN-LIKE BIOLOGICAL ACTIVITY. INTERACTS
CC       WITH THE EXENDIN RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Produced by the venomous gland.
CC   -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U77613; AAB51130.1; -.
DR   PIR; A42486; HWGH4G.
DR   InterPro; IPR000532; Glucagon.
DR   Pfam; PF00123; hormone2; 1.
DR   SMART; SM00070; GLUCA; 1.
DR   PROSITE; PS00260; GLUCAGON; 1.
KW   Glucagon family; Toxin; Amidation; Signal.
FT   SIGNAL       1     23       POTENTIAL.
FT   PEPTIDE      48    86       EXENDIN-4.
FT   MOD_RES      86    86       AMIDATION (G-87 PROVIDE AMIDE GROUP).
SQ   SEQUENCE   87 AA;  9479 MW;  656BA6E3D87454A2 CRC64;

  Query Match             61.2%;  Score 68.5;  DB 1;  Length 87;
  Best Local Similarity   59.4%;  Pred. No. 3.6e-06;
  Matches   19;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db         51 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 82


RESULT 3
CPXP_BRAJA
ID   CPXP_BRAJA     STANDARD;      PRT;   401 AA.
AC   Q59203;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Cytochrome P450 BJ-1 (EC 1.14.14.-) (Cytochrome P450 112).
GN   CYP112.
OS   Bradyrhizobium japonicum.
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Bradyrhizobium group; Bradyrhizobium.
OX   NCBI_TaxID=375;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=USDA 110;
RA   Tully R.E., Keister D.L.;
RT   "Cloning and mutagenesis of a cytochrome P-450 locus from
RT   Bradyrhizobium japonicum that is expressed anaerobically and
RT   symbiotically.";
RL   Appl. Environ. Microbiol. 59:4136-4142(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=USDA 110;
RX   MEDLINE=98322110; PubMed=9655913;
RA   Tully R.E., van Berkum P., Lovins K.W., Keister D.L.;
RT   "Identification and sequencing of a cytochrome P450 gene cluster from
RT   Bradyrhizobium japonicum.";
RL   Biochim. Biophys. Acta 1398:243-255(1998).
CC   -!- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC       MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED
CC       COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.
CC   -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U12678; AAC28889.1; -.
DR   HSSP; Q00441; 1OXA.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   Pfam; PF00067; p450; 1.
DR   PROSITE; PS00086; CYTOCHROME_P450; 1.
KW   Oxidoreductase; Monooxygenase; Electron transport; Heme.
FT   BINDING     350    350       HEME (BY SIMILARITY).
SQ   SEQUENCE   401 AA;  44496 MW;  869F2D0D087D9AB7 CRC64;

  Query Match             34.8%;  Score 39;  DB 1;  Length 401;
  Best Local Similarity   47.6%;  Pred. No. 6.7;
  Matches   10;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLXGGXSS 32
              |  ||||| |    |  |  |
Db        221 KASEEEAVGLAAGMLVAGHES 241


RESULT 4
YFDC_ECOLI
ID   YFDC_ECOLI     STANDARD;      PRT;   310 AA.
AC   P37327;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Hypothetical protein yfdC.
GN   YFDC OR B2347.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12;
RA   Baumann S.;
RL   Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=97426617; PubMed=9278503;
RA   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA   Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA   Mau B., Shao Y.;
RT   "The complete genome sequence of Escherichia coli K-12.";
RL   Science 277:1453-1474(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12;
RX   MEDLINE=97349980; PubMed=9205837;
RA   Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
```

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OM protein - protein search, using sw model

Run on: June 24, 2003, 22:59:44 ; Search time 13 Seconds
(without alignments)
127.619 Million cell updates/sec

Title: US-09-889-331A-48
Perfect score: 112
Sequence: 1 XXXGTXXXXXSKQXEEEAVRLXXXXLXGGXSSGAXXXXXX 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	68.5	61.2	39	1	EXE3_HELHO	P20394 heloderma h
2	68.5	61.2	87	1	EXE4_HELSU	P26349 heloderma s
3	39	34.8	401	1	CPXP_BRAJA	Q59203 bradyrhizob
4	38	33.9	310	1	YFDC_ECOLI	P37327 escherichia
5	38	33.9	512	1	Y4WA_RHISN	P55679 rhizobium s
6	37	33.0	248	1	PCRB_METTH	O26652 methanobact
7	37	33.0	449	1	CMGA_BOVIN	P05059 bos taurus
8	37	33.0	536	1	ANPC_MOUSE	P70180 mus musculu
9	36	32.1	251	1	C561_HUMAN	P49447 homo sapien
10	36	32.1	344	1	VU79_HSV6U	P52529 human herpe
11	36	32.1	784	1	SP4_HUMAN	Q02446 homo sapien
12	36	32.1	823	1	NUC1_NEUCR	P20824 neurospora
13	36	32.1	1049	1	CARB_SULTO	Q970u7 sulfolobus
14	36	32.1	3068	1	POLG_PEMVC	Q01500 p genome po
15	35.5	31.7	382	1	FTSZ_BACSU	P17865 bacillus su
16	35	31.2	300	1	TF2B_PYRAB	Q9v0v5 pyrococcus
17	35	31.2	300	1	TF2B_PYRHO	O59151 pyrococcus
18	35	31.2	338	1	FLIG_PSEAE	Q51464 pseudomonas
19	35	31.2	563	1	IDS_MOUSE	Q08890 mus musculu
20	35	31.2	1192	1	LMG2_MOUSE	Q61092 mus musculu
21	35	31.2	1262	1	MYO6_HUMAN	Q9um54 homo sapien
22	35	31.2	1265	1	MYO6_MOUSE	Q64331 mus musculu
23	34	30.4	85	1	YH74_YERPE	Q8zfe0 yersinia pe
24	34	30.4	248	1	TPIS_MACMU	P15426 macaca mula
25	34	30.4	400	1	CPXP_RHISN	P55544 rhizobium s
26	34	30.4	485	1	VG14_BPMD2	O64207 mycobacteri
27	34	30.4	535	1	ANPC_RAT	P41740 rattus norv
28	34	30.4	620	1	Y886_METJA	Q58296 methanococc
29	34	30.4	665	1	ENV_MLVMO	P03385 moloney mur
30	34	30.4	673	1	Y552_HUMAN	O60299 homo sapien
31	34	30.4	723	1	HR96_DROME	Q24143 drosophila
32	34	30.4	862	1	CNRC_CHICK	P52731 gallus gall
33	34	30.4	982	1	LI10_CAEEL	O17583 caenorhabdi
34	34	30.4	1097	1	KF1D_RAT	O35787 rattus norv
35	34	30.4	1103	1	KF1C_HUMAN	O43896 homo sapien
36	34	30.4	1905	1	TAGB_DICDI	P54683 dictyosteli
37	33	29.5	135	1	RK16_GRATE	P16633 gracilaria
38	33	29.5	289	1	TXNL_HUMAN	O43396 homo sapien
39	33	29.5	316	1	YE85_MYCPN	P75300 mycoplasma
40	33	29.5	337	1	LPLA_ECOLI	P32099 escherichia
41	33	29.5	378	1	RECA_FUSNN	Q8rfy0 fusobacteri
42	33	29.5	466	1	VP19_HSV2G	P22486 herpes simp
43	33	29.5	466	1	VP19_HSV2H	P89461 herpes simp
44	33	29.5	482	1	NODT_RHILV	P15727 rhizobium l
45	33	29.5	609	1	VG16_BPP22	Q01146 bacteriopha

ALIGNMENTS

RESULT 1
EXE3_HELHO
ID EXE3_HELHO STANDARD; PRT; 39 AA.
AC P20394;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Exendin-3.
OS Heloderma horridum horridum (Mexican beaded lizard).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Helodermatidae;
OC Heloderma.
OX NCBI_TaxID=8552;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=91056067; PubMed=1700785;
RA Eng J., Andrew P.C., Kleinman W.A., Singh L., Raufman J.-P.;
RT "Purification and structure of exendin-3, a new pancreatic
RT secretagogue isolated from Heloderma horridum venom.";
RL J. Biol. Chem. 265:20259-20262(1990).
CC -!- FUNCTION: HAS A VIP/SECRETIN-LIKE BIOLOGICAL ACTIVITY. INTERACTS
CC WITH THE EXENDIN RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Produced by the venomous gland.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR PIR; A23674; HWGH3Z.
DR HSSP; P01275; 1BH0.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 1.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Toxin; Amidation.
FT MOD_RES 39 39 AMIDATION.
SQ SEQUENCE 39 AA; 4204 MW; A44251D3A4B1D1B9 CRC64;

Query Match 61.2%; Score 68.5; DB 1; Length 39;
Best Local Similarity 59.4%; Pred. No. 1.5e-06;
Matches 19; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

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Qy          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
              ||     ||| |||||||    |  || ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35
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RESULT 2
EXE4_HELSU
ID EXE4_HELSU STANDARD; PRT; 87 AA.
AC P26349;
DT 01-MAY-1992 (Rel. 22, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Exendin-4 precursor.
OS Heloderma suspectum (Gila monster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Helodermatidae;

```
DR   InterPro; IPR001092; HLH_basic.
DR   Pfam; PF00010; HLH; 1.
DR   SMART; SM00353; HLH; 1.
DR   PROSITE; PS00038; HLH_1; 1.
DR   PROSITE; PS50888; HLH_2; 1.
KW   DNA-binding; Nuclear protein; Transcription regulation; Activator;
KW   Neurogenesis; Developmental protein; Differentiation.
FT   DOMAIN       58     77       GLU-RICH (ACIDIC).
FT   DOMAIN       87     93       NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT   DNA_BIND    102    113       BASIC DOMAIN.
FT   DOMAIN      114    154       HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
FT   DOMAIN       67     76       POLY-GLU.
FT   DOMAIN       87     90       POLY-LYS.
SQ   SEQUENCE   357 AA;  40000 MW;  F773637E64D3E99E CRC64;

  Query Match             31.4%;  Score 38;  DB 1;  Length 357;
  Best Local Similarity   42.1%;  Pred. No. 22;
  Matches    8;  Conservative    3;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLKNGG 30
              |: | ||:      |:|||
Db         39 KEDELEAMNAEEDSLRNGG 57


Search completed: June 24, 2003, 23:05:51
Job time : 14 secs
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CC   ---------------------------------------------------------------------
DR   EMBL; U24679; AAA86518.1; ALT_INIT.
DR   InterPro; IPR001092; HLH_basic.
DR   Pfam; PF00010; HLH; 1.
DR   SMART; SM00353; HLH; 1.
DR   PROSITE; PS00038; HLH_1; 1.
DR   PROSITE; PS50888; HLH_2; 1.
KW   DNA-binding; Nuclear protein; Transcription regulation; Activator;
KW   Neurogenesis; Developmental protein; Differentiation.
FT   DOMAIN       58     77       GLU-RICH (ACIDIC).
FT   DOMAIN       86     92       NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT   DNA_BIND    101    112       BASIC DOMAIN.
FT   DOMAIN      113    153       HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
FT   DOMAIN       67     75       POLY-GLU.
FT   DOMAIN       86     89       POLY-LYS.
SQ   SEQUENCE   355 AA;  39763 MW;  F4344DFD360226B2 CRC64;

  Query Match             31.4%;  Score 38;  DB 1;  Length 355;
  Best Local Similarity   42.1%;  Pred. No. 21;
  Matches    8;  Conservative    3;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLKNGG 30
              |: | ||:      |:|||
Db         39 KEDELEAMNAEEDSLRNGG 57


RESULT 14
NDF1_MOUSE
ID   NDF1_MOUSE     STANDARD;      PRT;   357 AA.
AC   Q60867; Q60897;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Neurogenic differentiation factor 1 (NeuroD1).
GN   NEUROD1 OR NEUROD.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MF1, and 129/Sv;
RX   MEDLINE=95273957; PubMed=7754368;
RA   Lee J.E., Hollenberg S.M., Snider L., Turner D.L., Lipnick N.,
RA   Weintraub H.;
RT   "Conversion of Xenopus ectoderm into neurons by NeuroD, a basic
RT   helix-loop-helix protein.";
RL   Science 268:836-844(1995).
CC   -!- FUNCTION: ACTS AS A DIFFERENTIATION FACTOR DURING NEUROGENESIS.
CC       TRANSCRIPTIONAL ACTIVATOR. BINDS TO THE INSULIN GENE E-BOX.
CC   -!- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
CC       BHLH PROTEIN. HETERODIMER WITH E47.
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN DIFFERENTIATING NEURONS OF
CC       BOTH THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYONIC DEVELOPMENT.
CC   -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC       TRANSCRIPTION FACTORS. "ATONAL" SUBFAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U28068; AAC52203.1; -.
DR   EMBL; U28888; AAC52204.1; -.
DR   MGD; MGI:1339708; Neurod1.
DR   InterPro; IPR001092; HLH_basic.
DR   Pfam; PF00010; HLH; 1.
DR   SMART; SM00353; HLH; 1.
DR   PROSITE; PS00038; HLH_1; 1.
DR   PROSITE; PS50888; HLH_2; 1.
KW   DNA-binding; Nuclear protein; Transcription regulation; Activator;
KW   Neurogenesis; Developmental protein; Differentiation.
FT   DOMAIN       58     77       GLU-RICH (ACIDIC).
FT   DOMAIN       87     93       NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT   DNA_BIND    102    113       BASIC DOMAIN.
FT   DOMAIN      114    154       HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
FT   DOMAIN       58     64       POLY-GLU.
FT   DOMAIN       67     77       POLY-GLU.
FT   DOMAIN       87     90       POLY-LYS.
SQ   SEQUENCE   357 AA;  39998 MW;  B6626E1315E31027 CRC64;

  Query Match             31.4%;  Score 38;  DB 1;  Length 357;
  Best Local Similarity   42.1%;  Pred. No. 22;
  Matches    8;  Conservative    3;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLKNGG 30
              |: | ||:      |:|||
Db         39 KEDELEAMNAEEDSLRNGG 57


RESULT 15
NDF1_RAT
ID   NDF1_RAT       STANDARD;      PRT;   357 AA.
AC   Q64289;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Neurogenic differentiation factor 1 (NeuroD1) (Basic helix-loop-helix
DE   factor 1) (BHF-1).
GN   NEUROD1 OR NEUROD.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cerebellum;
RX   MEDLINE=96220182; PubMed=8660336;
RA   Kawakami H., Maruyama H., Yasunami M., Ohkubo H., Hara H., Saida T.,
RA   Nakanishi S., Nakamura S.;
RT   "Cloning and expression of a rat brain basic helix-loop-helix
RT   factor.";
RL   Biochem. Biophys. Res. Commun. 221:199-204(1996).
RN   [2]
RP   SEQUENCE OF 88-200 FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Retina;
RA   Ahmad I., Acharay H.R.;
RL   Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: ACTS AS A DIFFERENTIATION FACTOR DURING NEUROGENESIS.
CC       TRANSCRIPTIONAL ACTIVATOR. BINDS TO THE INSULIN GENE E-BOX.
CC   -!- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
CC       BHLH PROTEIN. HETERODIMER WITH E47.
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC       TRANSCRIPTION FACTORS. "ATONAL" SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D82075; BAA11536.1; -.
DR   EMBL; D82074; BAA11535.1; -.
DR   EMBL; U80603; AAB38744.1; -.
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RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: STABILIZES TBP BINDING TO AN ARCHAEAL BOX-A PROMOTER.
CC       ALSO RESPONSIBLE FOR RECRUITING RNA POLYMERASE II TO THE PRE-
CC       INITIATION COMPLEX (DNA-TBP-TFIIB) (BY SIMILARITY).
CC   -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE TFIIB FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ248285; CAB49598.1; -.
DR   HSSP; P29095; 1AIS.
DR   InterPro; IPR004366; Cyclin.
DR   InterPro; IPR000812; TFIIB_euk.
DR   Pfam; PF00382; transcript_fac2; 2.
DR   PRINTS; PR00685; TIFACTORIIB.
DR   SMART; SM00385; CYCLIN; 2.
DR   PROSITE; PS00782; TFIIB; 2.
KW   Transcription regulation; Repeat; Zinc-finger; Metal-binding; Zinc;
KW   Complete proteome.
FT   ZN_FING       7     29       ZN-RIBBON TFIIB-TYPE.
FT   REPEAT      114    197       1.
FT   REPEAT      210    291       2.
FT   METAL         7      7       ZINC (BY SIMILARITY).
FT   METAL        10     10       ZINC (BY SIMILARITY).
FT   METAL        26     26       ZINC (BY SIMILARITY).
FT   METAL        29     29       ZINC (BY SIMILARITY).
SQ   SEQUENCE   300 AA;  34069 MW;  D7AE15181A36BD4F CRC64;

  Query Match             31.4%;  Score 38;  DB 1;  Length 300;
  Best Local Similarity   44.4%;  Pred. No. 18;
  Matches    8;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLKNG 29
              |  |||| ||    :: |
Db        127 KHVEEEAARLYREAVRKG 144


RESULT 12
TF2B_PYRHO
ID   TF2B_PYRHO     STANDARD;      PRT;   300 AA.
AC   O59151;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Transcription initiation factor IIB (TFIIB).
GN   TFB OR PH1482.
OS   Pyrococcus horikoshii.
OC   Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC   Pyrococcus.
OX   NCBI_TaxID=53953;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=OT3;
RX   MEDLINE=98344137; PubMed=9679194;
RA   Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA   Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA   Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA   Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA   Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA   Masuchi Y., Shizuya H., Kikuchi H.;
RT   "Complete sequence and gene organization of the genome of a hyper-
RT   thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
RL   DNA Res. 5:55-76(1998).
CC   -!- FUNCTION: STABILIZES TBP BINDING TO AN ARCHAEAL BOX-A PROMOTER.
CC       ALSO RESPONSIBLE FOR RECRUITING RNA POLYMERASE II TO THE PRE-
CC       INITIATION COMPLEX (DNA-TBP-TFIIB) (BY SIMILARITY).
CC   -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE TFIIB FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AP000006; BAA30589.1; -.
DR   HSSP; P29095; 1AIS.
DR   InterPro; IPR004366; Cyclin.
DR   InterPro; IPR000812; TFIIB_euk.
DR   Pfam; PF00382; transcript_fac2; 2.
DR   PRINTS; PR00685; TIFACTORIIB.
DR   SMART; SM00385; CYCLIN; 2.
DR   PROSITE; PS00782; TFIIB; 2.
KW   Transcription regulation; Repeat; Zinc-finger; Metal-binding; Zinc;
KW   Complete proteome.
FT   ZN_FING       7     29       ZN-RIBBON TFIIB-TYPE.
FT   REPEAT      114    197       1.
FT   REPEAT      210    291       2.
FT   METAL         7      7       ZINC (BY SIMILARITY).
FT   METAL        10     10       ZINC (BY SIMILARITY).
FT   METAL        26     26       ZINC (BY SIMILARITY).
FT   METAL        29     29       ZINC (BY SIMILARITY).
SQ   SEQUENCE   300 AA;  34097 MW;  DE9758F398BC855F CRC64;

  Query Match             31.4%;  Score 38;  DB 1;  Length 300;
  Best Local Similarity   44.4%;  Pred. No. 18;
  Matches    8;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLKNG 29
              |  |||| ||    :: |
Db        127 KHVEEEAARLYREAVRKG 144


RESULT 13
NDF1_MESAU
ID   NDF1_MESAU     STANDARD;      PRT;   355 AA.
AC   Q60430;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Neurogenic differentiation factor 1 (NeuroD1) (Beta-cell E-box trans-
DE   activator 2) (BETA2).
GN   NEUROD1 OR NEUROD.
OS   Mesocricetus auratus (Golden hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Mesocricetus.
OX   NCBI_TaxID=10036;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95293222; PubMed=7774807;
RA   Naya F.J., Stellrecht C.M.M., Tsai M.-J.;
RT   "Tissue-specific regulation of the insulin gene by a novel basic
RT   helix-loop-helix transcription factor.";
RL   Genes Dev. 9:1009-1019(1995).
CC   -!- FUNCTION: ACTS AS A DIFFERENTIATION FACTOR DURING NEUROGENESIS.
CC       TRANSCRIPTIONAL ACTIVATOR. BINDS TO THE INSULIN GENE E-BOX.
CC   -!- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
CC       BHLH PROTEIN. HETERODIMER WITH E47.
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- TISSUE SPECIFICITY: MOST ABUNDANT IN PANCREATIC ALPHA- AND BETA-
CC       CELLS, LESS IN BRAIN AND INTESTINE.
CC   -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC       TRANSCRIPTION FACTORS. "ATONAL" SUBFAMILY.
CC   ---------------------------------------------------------------------
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SQ   SEQUENCE   2064 AA;  230489 MW;  D3BDCC10A94D9E6C CRC64;

  Query Match             33.9%;  Score 41;  DB 1;  Length 2064;
  Best Local Similarity   41.7%;  Pred. No. 39;
  Matches   10;  Conservative    4;  Mismatches   10;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLKNGGXSSGA 35
              :|   |:||     :|| | |||:
Db       1781 RQIIRESVRNMSIPMKNFGGSSGS 1804


RESULT 9
TRL3_HUMAN
ID   TRL3_HUMAN     STANDARD;      PRT;  1017 AA.
AC   Q9HCF6;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Long transient receptor potential channel 3 (LTrpC3) (Fragment).
GN   TRPM3 OR LTRPC3 OR KIAA1616.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=20450683; PubMed=10997877;
RA   Nagase T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes.
RT   XVIII. The complete sequences of 100 new cDNA clones from brain which
RT   code for large proteins in vitro.";
RL   DNA Res. 7:273-281(2000).
CC   -!- FUNCTION: MAY BE A CALCIUM CHANNEL.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC   -!- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. LTRPC
CC       SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB046836; BAB13442.1; -.
DR   Genew; HGNC:17992; TRPM3.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR000636; M+channel_nlg.
DR   Pfam; PF00520; ion_trans; 1.
KW   Ionic channel; Transmembrane; Ion transport; Calcium channel.
FT   NON_TER       1      1
FT   TRANSMEM     80    100       POTENTIAL.
FT   TRANSMEM    183    203       POTENTIAL.
FT   TRANSMEM    250    270       POTENTIAL.
FT   TRANSMEM    314    334       POTENTIAL.
FT   TRANSMEM    402    422       POTENTIAL.
FT   TRANSMEM    453    473       POTENTIAL.
SQ   SEQUENCE   1017 AA;  116681 MW;  B088354F100A972C CRC64;

  Query Match             33.1%;  Score 40;  DB 1;  Length 1017;
  Best Local Similarity   39.1%;  Pred. No. 28;
  Matches    9;  Conservative    4;  Mismatches   10;  Indels    0;  Gaps    0;

Qy         11 SKQXEEEAVRLXXXXLKNGGXSS 33
              :|: ||| : |     :| | ||
Db       129 TKEKEEEDMELTAMLGRNNGESS 151


RESULT 10
HRPZ_PSESY
ID   HRPZ_PSESY     STANDARD;      PRT;   341 AA.
AC   P35674;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Harpin-PSS.
GN   HRPZ.
OS   Pseudomonas syringae (pv. syringae).
OC   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC   Pseudomonas.
OX   NCBI_TaxID=321;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 141-162.
RC   STRAIN=61;
RX   MEDLINE=93313957; PubMed=8324821;
RA   He S.Y., Huang H.-C., Collmer A.;
RT   "Pseudomonas syringae pv. syringae harpinPss: a protein that is
RT   secreted via the Hrp pathway and elicits the hypersensitive response
RT   in plants.";
RL   Cell 73:1255-1266(1993).
CC   -!- FUNCTION: ELICITS THE HYPERSENSITIVE RESPONSE (HR) IN THE PLANT
CC       UPON INFECTION. HARPIN ELICITS HR IN NON-HOSTS AND IS ALSO
CC       REQUIRED FOR PATHOGENICITY IN HOST PLANTS.
CC   -!- SUBCELLULAR LOCATION: SECRETED; VIA THE HRP SECRETION PATHWAY.
CC   -!- MISCELLANEOUS: DIFFERENT PLANTS EXHIBIT DIFFERENT LEVELS OF
CC       SENSITIVITY TO HARPIN-PSS.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L14775; AAA25839.1; -.
DR   PIR; A40706; A40706.
KW   Hypersensitive response; Repeat.
FT   DOMAIN      210    271       2 X 7 AA REPEATS OF G-G-G-L-G-T-P.
FT   REPEAT      210    216       1-1.
FT   REPEAT      265    271       1-2.
FT   DOMAIN      276    314       2 X 4 AA REPEATS OF Q-T-G-T.
FT   REPEAT      276    279       2-1.
FT   REPEAT      311    314       2-2.
SQ   SEQUENCE   341 AA;  34721 MW;  75FB7329B5380179 CRC64;

  Query Match             32.2%;  Score 39;  DB 1;  Length 341;
  Best Local Similarity   32.0%;  Pred. No. 14;
  Matches    8;  Conservative    4;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          5 TXXXXXSKQXEEEAVRLXXXXLKNG 29
              |     ||  :|  |:|    ::||
Db         27 TTGSTSSKALQEVVVKLAEELMRNG 51


RESULT 11
TF2B_PYRAB
ID   TF2B_PYRAB     STANDARD;      PRT;   300 AA.
AC   Q9V0V5;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Transcription initiation factor IIB (TFIIB).
GN   TFB OR PAB1912.
OS   Pyrococcus abyssi.
OC   Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC   Pyrococcus.
OX   NCBI_TaxID=29292;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GE5 / Orsay;
RA   Heilig R.;
RT   "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
RT   structure and evolution.";
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```
CC       SEGMENT OF THE CENTRAL NERVOUS SYSTEM. AT STAGE 17, EXPRESSION
CC       BECOMES RESTRICTED TO THE SYNAPTIC REGIONS OF THE BRAIN AND
CC       VENTRAL NERVE CORD, WHERE SYNAPSES UNDERGO MATURATION.
CC   -!- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY (DH) DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
CC   -!- SIMILARITY: CONTAINS 2 PH DOMAINS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D86546; BAA13108.1; -.
DR   HSSP; P08567; 1PLS.
DR   FlyBase; FBgn0019652; sif.
DR   InterPro; IPR001331; GDS_CDC24.
DR   InterPro; IPR001478; PDZ.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR003116; RBD.
DR   InterPro; IPR000219; RhoGEF.
DR   Pfam; PF00169; PH; 2.
DR   Pfam; PF00621; RhoGEF; 1.
DR   Pfam; PF02196; RBD; 1.
DR   SMART; SM00228; PDZ; 1.
DR   SMART; SM00233; PH; 2.
DR   SMART; SM00455; RBD; 1.
DR   SMART; SM00325; RhoGEF; 1.
DR   PROSITE; PS50010; DH_2; 1.
DR   PROSITE; PS00741; DH_1; 1.
DR   PROSITE; PS50106; PDZ; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
KW   Guanine-nucleotide releasing factor; Developmental protein; Synapse;
KW   Repeat; Alternative splicing.
FT   DOMAIN       62    249       4 X 25 AA APPROXIMATE REPEAT.
FT   REPEAT       62     86       1.
FT   REPEAT       94    118       2.
FT   REPEAT      154    178       3.
FT   REPEAT      225    249       4.
FT   DOMAIN      819    937       PH 1.
FT   DOMAIN     1184   1273       PDZ.
FT   DOMAIN     1408   1602       DH.
FT   DOMAIN     1674   1767       PH 2.
FT   DOMAIN      467    470       POLY-PRO.
FT   DOMAIN      646    649       POLY-ARG.
FT   DOMAIN     1295   1298       POLY-PRO.
FT   DOMAIN     1898   1909       POLY-GLN.
FT   DOMAIN     1929   1933       POLY-PRO.
SQ   SEQUENCE   2044 AA;  228324 MW;  75D7CF21F49654B6 CRC64;

  Query Match             33.9%;  Score 41;  DB 1;  Length 2044;
  Best Local Similarity   41.7%;  Pred. No. 38;
  Matches   10;  Conservative    4;  Mismatches   10;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLKNGGXSSGA 35
              :|   |:||     :|| | |||:
Db       1761 RQIIRESVRNMSIPMKNFGGSSGS 1784


RESULT 8
SIF1_DROME
ID   SIF1_DROME     STANDARD;      PRT;  2064 AA.
AC   P91621;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Still life protein type 1 (SIF type 1).
GN   SIF.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC   Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Head;
RX   MEDLINE=97153054; PubMed=8999801;
RA   Sone M., Hoshino M., Suzuki E., Kuroda S., Kaibuchi K., Nakagoshi H.,
RA   Saigo K., Nabeshima Y.-I., Hama C.;
RT   "Still life, a protein in synaptic terminals of Drosophila homologous
RT   to GDP-GTP exchangers.";
RL   Science 275:543-547(1997).
RN   [2]
RP   ERRATUM.
RA   Sone M., Hoshino M., Suzuki E., Kuroda S., Kaibuchi K., Nakagoshi H.,
RA   Saigo K., Nabeshima Y.-I., Hama C.;
RL   Science 275:1405-1405(1997).
CC   -!- FUNCTION: REGULATES SYNAPTIC DIFFERENTIATION THROUGH THE
CC       ORGANIZATION OF ACTIN CYTOSKELETON POSSIBLY BY ACTIVATING RHO-LIKE
CC       GTPASES. IS LIKELY A FACTOR IN THE CASCADE OF RAC1 OR CDC42 IN THE
CC       NEURONS.
CC   -!- SUBCELLULAR LOCATION: LOCALIZES TO THE SUBMEMBRANOUS REGION OF
CC       SYNAPTIC TERMINALS.
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; SIF TYPE 1 (SHOWN HERE) AND SIF
CC       TYPE 2 (AC P91620); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- DEVELOPMENTAL STAGE: AT STAGE 14, EXPRESSION OCCURS IN EACH
CC       SEGMENT OF THE CENTRAL NERVOUS SYSTEM. AT STAGE 17, EXPRESSION
CC       BECOMES RESTRICTED TO THE SYNAPTIC REGIONS OF THE BRAIN AND
CC       VENTRAL NERVE CORD, WHERE SYNAPSES UNDERGO MATURATION.
CC   -!- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY (DH) DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
CC   -!- SIMILARITY: CONTAINS 2 PH DOMAINS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D86547; BAA13109.1; -.
DR   HSSP; P08567; 1PLS.
DR   FlyBase; FBgn0019652; sif.
DR   InterPro; IPR001331; GDS_CDC24.
DR   InterPro; IPR001478; PDZ.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR003116; RBD.
DR   InterPro; IPR000219; RhoGEF.
DR   InterPro; IPR001960; WH1.
DR   Pfam; PF00169; PH; 2.
DR   Pfam; PF00621; RhoGEF; 1.
DR   Pfam; PF02196; RBD; 1.
DR   SMART; SM00228; PDZ; 1.
DR   SMART; SM00233; PH; 2.
DR   SMART; SM00455; RBD; 1.
DR   SMART; SM00325; RhoGEF; 1.
DR   SMART; SM00461; WH1; 1.
DR   PROSITE; PS50010; DH_2; 1.
DR   PROSITE; PS00741; DH_1; 1.
DR   PROSITE; PS50106; PDZ; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
KW   Guanine-nucleotide releasing factor; Developmental protein; Repeat;
KW   Myristate; Synapse; Alternative splicing.
FT   LIPID         2      2       MYRISTATE (POTENTIAL).
FT   DOMAIN      839    957       PH 1.
FT   DOMAIN     1204   1293       PDZ.
FT   DOMAIN     1428   1622       DH.
FT   DOMAIN     1694   1787       PH 2.
FT   DOMAIN      445    453       POLY-GLY.
FT   DOMAIN      545    548       POLY-GLN.
FT   DOMAIN     1315   1318       POLY-PRO.
FT   DOMAIN     1918   1929       POLY-GLN.
FT   DOMAIN     1949   1953       POLY-PRO.
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DR   MIM; 605173; -.
DR   InterPro; IPR000210; BTB_POZ.
DR   InterPro; IPR001798; Kelch.
DR   Pfam; PF00651; BTB; 1.
DR   Pfam; PF01344; Kelch; 5.
DR   SMART; SM00225; BTB; 1.
DR   PROSITE; PS50097; BTB; 1.
KW   Actin-binding; Developmental protein; Cytoskeleton; Repeat;
KW   Phosphorylation.
FT   DOMAIN       46    114       BTB.
FT   REPEAT      296    340       KELCH 1.
FT   REPEAT      341    388       KELCH 2.
FT   REPEAT      389    444       KELCH 3.
FT   REPEAT      446    492       KELCH 4.
FT   REPEAT      494    538       KELCH 5.
FT   REPEAT      539    585       KELCH 6.
FT   CONFLICT    112    130       INEENAESLLEAGDMLEFQ -> HQLEGKCRNSLLGSLVTC
FT                                WSFK (IN REF. 1).
FT   CONFLICT    237    238       RL -> TR (IN REF. 1).
FT   CONFLICT    402    402       C -> S (IN REF. 2).
FT   CONFLICT    427    427       V -> A (IN REF. 1).
FT   CONFLICT    430    438       LREGVSNAA -> RPRRRYNCAQ (IN REF. 1).
FT   CONFLICT    484    589       YTAAAVLGNQIFIMGGDTEFSACSAYKFNSETYQWTKVGDV
FT                                TAKRMSCHAVASGNKLYVVGGYFGIQRCKTLDCYDPTLDVW
FT                                NSITTVPYSLIPTAFVSTWKHLPS -> IHSQASCPGGTQD
FT                                FLLWGVIQNFSACFCL (IN REF. 1).
SQ   SEQUENCE   589 AA;  66129 MW;  DB003A1DFA65BAA0 CRC64;

  Query Match             33.9%;  Score 41;  DB 1;  Length 589;
  Best Local Similarity   45.0%;  Pred. No. 11;
  Matches    9;  Conservative    3;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         11 SKQXEEEAVRLXXXXLKNGG 30
              ||:  |||:|     |:| |
Db        262 SKEIVEEAIRCKLKILQNDG 281


RESULT 6
ENC1_MOUSE
ID   ENC1_MOUSE     STANDARD;      PRT;   589 AA.
AC   O35709;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Ectoderm-neural cortex-1 protein (ENC-1).
GN   ENC1 OR ENC-1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Swiss albino; TISSUE=Brain;
RX   MEDLINE=97252647; PubMed=9096139;
RA   Hernandez M.-C., Andres-Barquin P.J., Martinez S., Bulfone A.,
RA   Rubenstein J.L.R., Israel M.A.;
RT   "ENC-1: a novel mammalian kelch-related gene specifically expressed in
RT   the nervous system encodes an actin-binding protein.";
RL   J. Neurosci. 17:3038-3051(1997).
CC   -!- FUNCTION: ACTIN-BINDING PROTEIN INVOLVED IN THE REGULATION OF
CC       NEURONAL PROCESS FORMATION AND IN DIFFERENTIATION OF NEURAL CREST
CC       CELLS.
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC. INTERACTS WITH THE ACTIN
CC       CYTOSKELETON.
CC   -!- TISSUE SPECIFICITY: PRIMARILY EXPRESSED IN THE NERVOUS SYSTEM.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSION IS HIGHLY DYNAMIC BUT MOSTLY
CC       RESTRICTED TO THE NS. OUTSIDE THE NS, EXPRESSION IS DETECTED IN
CC       THE ROSTRAL-MOST SOMITOMERE OF THE PRESOMITIC MESODERM, AT THE
CC       TIMES CORRESPONDING TO THE EPITHELIALIZATION THAT PRECEDES SOMITE
CC       FORMATION. FIRST DETECTED IN THE BRAIN AND SPINAL CHORD OF 12 PC
CC       EMBRYOS.
CC   -!- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
CC   -!- SIMILARITY: CONTAINS 6 KELCH REPEATS.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U65079; AAB64206.1; -.
DR   MGD; MGI:109610; Enc1.
DR   InterPro; IPR000210; BTB_POZ.
DR   InterPro; IPR001798; Kelch.
DR   Pfam; PF00651; BTB; 1.
DR   Pfam; PF01344; Kelch; 5.
DR   SMART; SM00225; BTB; 1.
DR   PROSITE; PS50097; BTB; 1.
KW   Actin-binding; Developmental protein; Cytoskeleton; Repeat.
FT   DOMAIN       46    114       BTB.
FT   REPEAT      296    340       KELCH 1.
FT   REPEAT      341    388       KELCH 2.
FT   REPEAT      389    444       KELCH 3.
FT   REPEAT      446    492       KELCH 4.
FT   REPEAT      494    538       KELCH 5.
FT   REPEAT      539    585       KELCH 6.
SQ   SEQUENCE   589 AA;  66085 MW;  12E62354D508B6A2 CRC64;

  Query Match             33.9%;  Score 41;  DB 1;  Length 589;
  Best Local Similarity   45.0%;  Pred. No. 11;
  Matches    9;  Conservative    3;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         11 SKQXEEEAVRLXXXXLKNGG 30
              ||:  |||:|     |:| |
Db        262 SKEIVEEAIRCKLKILQNDG 281


RESULT 7
SIF2_DROME
ID   SIF2_DROME     STANDARD;      PRT;  2044 AA.
AC   P91620;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Still life protein type 2 (SIF type 2).
GN   SIF.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC   Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Head;
RX   MEDLINE=97153054; PubMed=8999801;
RA   Sone M., Hoshino M., Suzuki E., Kuroda S., Kaibuchi K., Nakagoshi H.,
RA   Saigo K., Nabeshima Y.-I., Hama C.;
RT   "Still life, a protein in synaptic terminals of Drosophila homologous
RT   to GDP-GTP exchangers.";
RL   Science 275:543-547(1997).
RN   [2]
RP   ERRATUM.
RA   Sone M., Hoshino M., Suzuki E., Kuroda S., Kaibuchi K., Nakagoshi H.,
RA   Saigo K., Nabeshima Y.-I., Hama C.;
RL   Science 275:1405-1405(1997).
CC   -!- FUNCTION: REGULATES SYNAPTIC DIFFERENTIATION THROUGH THE
CC       ORGANIZATION OF ACTIN CYTOSKELETON POSSIBLY BY ACTIVATING RHO-LIKE
CC       GTPASES. IS LIKELY A FACTOR IN THE CASCADE OF RAC1 OR CDC42 IN THE
CC       NEURONS.
CC   -!- SUBCELLULAR LOCATION: LOCALIZES TO THE SUBMEMBRANOUS REGION OF
CC       SYNAPTIC TERMINALS.
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; SIF TYPE 1 (AC P91621) AND SIF
CC       TYPE 2 (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- DEVELOPMENTAL STAGE: AT STAGE 14, EXPRESSION OCCURS IN EACH
```

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Qy          12 KQXEEEAVRLXXXXLKN 28
               || |:||| :    |||
Db         529 KQIEKEAVEIVSEVLKN 545


RESULT 4
YFQB_SCHPO
ID   YFQB_SCHPO     STANDARD;      PRT;   357 AA.
AC   Q10170; Q9Y7I7;
DT   01-OCT-1996 (Rel. 34, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Hypothetical protein C8E11.11 in chromosome I.
GN   SPAC8E11.11 OR SPAC26A3.17C.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RX   MEDLINE=21848401; PubMed=11859360;
RA   Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA   Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA   Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA   Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA   Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA   Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA   James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA   Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA   Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA   Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA   Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA   Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA   Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA   Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA   Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA   Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA   Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA   Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA   Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA   Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA   Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA   Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA   Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA   Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT   "The genome sequence of Schizosaccharomyces pombe.";
RL   Nature 415:871-880(2002).
CC   -!- SIMILARITY: SOME, TO RAT GUANIDINOACETATE N-METHYLTRANSFERASE.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AL021817; CAB40198.1; -.
DR   EMBL; Z69240; CAA93240.1; -.
DR   InterPro; IPR002110; ANK.
KW   Hypothetical protein.
SQ   SEQUENCE   357 AA;  40709 MW;  5529B8D3B88D91A9 CRC64;

  Query Match             33.9%;  Score 41;  DB 1;  Length 357;
  Best Local Similarity   34.8%;  Pred. No. 6.3;
  Matches    8;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          12 KQXEEEAVRLXXXXLKNGGXSSG 34
               |: | :|: :    | |||  :|
Db          64 KETEVQAIEVTKWILSNGGVWNG 86
```

```
RESULT 5
ENC1_HUMAN
ID   ENC1_HUMAN     STANDARD;      PRT;   589 AA.
AC   O14682; Q9UPG9; O75464;
DT   30-MAY-2000 (Rel. 39, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Ectoderm-neural cortex-1 protein (ENC-1) (P53-induced protein 10)
DE   (Nuclear matrix protein NRP/B).
GN   ENC1 OR PIG10 OR NRPB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon cancer;
RX   MEDLINE=97449378; PubMed=9305847;
RA   Polyak K., Xia Y., Zweier J.L., Kinzler K.W., Vogelstein B.;
RT   "A model for p53-induced apoptosis.";
RL   Nature 389:300-305(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98350113; PubMed=9683534;
RA   Hernandez M.-C., Andres-Barquin P.J., Holt I., Israel M.A.;
RT   "Cloning of human ENC-1 and evaluation of its expression and
RT   regulation in nervous system tumors.";
RL   Exp. Cell Res. 242:470-477(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hippocampus, and Fetal brain;
RX   MEDLINE=98234394; PubMed=9566959;
RA   Kim T.-A., Lim J., Ota S., Raja S., Rogers R., Rivnay B., Avraham H.,
RA   Avraham S.;
RT   "NRP/B, a novel nuclear matrix protein, associates with p110(RB) and
RT   is involved in neuronal differentiation.";
RL   J. Cell Biol. 141:553-566(1998).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RA   Strausberg R.;
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: ACTIN-BINDING PROTEIN INVOLVED IN THE REGULATION OF
CC       NEURONAL PROCESS FORMATION AND IN DIFFERENTIATION OF NEURAL CREST
CC       CELLS. MAY BE DOWN-REGULATED IN NEUROBLASTOMA TUMORS.
CC   -!- SUBUNIT: BINDS TO RB1. HYPOPHOSPHORYLATED RB1 ASSOCIATES WITH ENC1
CC       DURING NEURONAL DIFFERENTIATION, WHILE HYPERPHOSPHORYLATED RB1
CC       ASSOCIATES WITH ENC1 IN NONDIFFERENTIATING CELLS.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR. NUCLEAR MATRIX-ASSOCIATED.
CC   -!- TISSUE SPECIFICITY: DETECTED IN FETAL BRAIN TISSUE, MODERATE
CC       EXPRESSION IN FETAL HEART, LUNG AND KIDNEY. HIGHLY EXPRESSED IN
CC       ADULT BRAIN, PARTICULARLY HIGH IN THE HIPPOCAMPUS AND
CC       AMYGDALA, AND SPINAL CHORD. DETECTABLE IN ADULT PANCREAS.
CC   -!- DEVELOPMENTAL STAGE: DRAMATICALLY UPREGULATED UPON NEURONAL
CC       DIFFERENTIATION.
CC   -!- PTM: PHOSPHORYLATED.
CC   -!- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
CC   -!- SIMILARITY: CONTAINS 6 KELCH REPEATS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF010314; AAC39532.1; -.
DR   EMBL; AF005381; AAC64498.1; -.
DR   EMBL; AF059611; AAC26109.1; -.
DR   EMBL; BC000418; AAH00418.1; -.
DR   Genew; HGNC:3345; ENC1.
```

```
OC   Heloderma.
OX   NCBI_TaxID=8554;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97172477; PubMed=9020121;
RA   Chen Y.E., Drucker D.J.;
RT   "Tissue-specific expression of unique mRNAs that encode proglucagon-
RT   derived peptides or exendin 4 in the lizard.";
RL   J. Biol. Chem. 272:4108-4115(1997).
RN   [2]
RP   SEQUENCE OF 48-86.
RC   TISSUE=Venom;
RX   MEDLINE=92218391; PubMed=1313797;
RA   Eng J., Kleinman W.A., Singh L., Singh G., Raufman J.-P.;
RT   "Isolation and characterization of exendin-4, an exendin-3 analogue,
RT   from Heloderma suspectum venom. Further evidence for an exendin
RT   receptor on dispersed acini from guinea pig pancreas.";
RL   J. Biol. Chem. 267:7402-7405(1992).
CC   -!- FUNCTION: HAS A VIP/SECRETIN-LIKE BIOLOGICAL ACTIVITY. INTERACTS
CC       WITH THE EXENDIN RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Produced by the venomous gland.
CC   -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U77613; AAB51130.1; -.
DR   PIR; A42486; HWGH4G.
DR   InterPro; IPR000532; Glucagon.
DR   Pfam; PF00123; hormone2; 1.
DR   SMART; SM00070; GLUCA; 1.
DR   PROSITE; PS00260; GLUCAGON; 1.
KW   Glucagon family; Toxin; Amidation; Signal.
FT   SIGNAL       1     23       POTENTIAL.
FT   PEPTIDE      48    86       EXENDIN-4.
FT   MOD_RES      86    86       AMIDATION (G-87 PROVIDE AMIDE GROUP).
SQ   SEQUENCE   87 AA;  9479 MW;  656BA6E3D87454A2 CRC64;

  Query Match             75.2%;  Score 91;  DB 1;  Length 87;
  Best Local Similarity   65.6%;  Pred. No. 1.8e-09;
  Matches   21;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| ||||||||    ||||| ||||
Db         51 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 82


RESULT 3
PGMU_ECOLI
ID   PGMU_ECOLI     STANDARD;      PRT;   546 AA.
AC   P36938;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Phosphoglucomutase (EC 5.4.2.2) (Glucose phosphomutase) (PGM).
GN   PGM OR B0688.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12;
RX   MEDLINE=94364967; PubMed=8083177;
RA   Lu M., Kleckner N.;
RT   "Molecular cloning and characterization of the pgm gene encoding
RT   phosphoglucomutase of Escherichia coli.";
RL   J. Bacteriol. 176:5847-5851(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=97426617; PubMed=9278503;
RA   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA   Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA   Mau B., Shao Y.;
RT   "The complete genome sequence of Escherichia coli K-12.";
RL   Science 277:1453-1474(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12;
RX   MEDLINE=97061202; PubMed=8905232;
RA   Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA   Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA   Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA   Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
RA   Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA   Yano M., Horiuchi T.;
RT   "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT   corresponding to the 12.7-28.0 min region on the linkage map.";
RL   DNA Res. 3:137-155(1996).
RN   [4]
RP   SEQUENCE OF 1-20 FROM N.A.
RC   STRAIN=K12;
RX   MEDLINE=94236686; PubMed=8011018;
RA   Lu M., Campbell J.L., Boye E., Kleckner N.;
RT   "SeqA: a negative modulator of replication initiation in E. coli.";
RL   Cell 77:413-426(1994).
RN   [5]
RP   CHARACTERIZATION.
RA   Joshi J.G., Handler P.;
RT   "Phosphoglucomutase. II. Purification and properties of
RT   phosphoglucomutase from Escherichia coli.";
RL   J. Biol. Chem. 239:2741-2751(1964).
CC   -!- FUNCTION: THIS ENZYME PARTICIPATES IN BOTH THE BREAKDOWN AND
CC       SYNTHESIS OF GLUCOSE.
CC   -!- CATALYTIC ACTIVITY: Alpha-D-glucose 1-phosphate = alpha-D-glucose
CC       6-phosphate.
CC   -!- SIMILARITY: BELONGS TO THE PHOSPHOHEXOSE MUTASES FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U08369; AAA57067.1; -.
DR   EMBL; AE000172; AAC73782.1; -.
DR   EMBL; D90707; BAA35337.1; -.
DR   EMBL; D90708; BAA35345.1; -.
DR   EMBL; U07651; -; NOT_ANNOTATED_CDS.
DR   EcoGene; EG12144; pgm.
DR   InterPro; IPR001485; PG/PMM_mutase.
DR   Pfam; PF00408; PGM_PMM; 1.
DR   Pfam; PF02878; PGM_PMM_I; 1.
DR   Pfam; PF02879; PGM_PMM_II; 1.
DR   Pfam; PF02880; PGM_PMM_III; 1.
DR   TIGRFAMs; TIGR01132; pgm; 1.
DR   PROSITE; PS00710; PGM_PMM; 1.
KW   Isomerase; Phosphorylation; Complete proteome.
FT   ACT_SITE    146    146       FORMS THE PHOSPHOSERINE INTERMEDIATE
FT                                (BY SIMILARITY).
SQ   SEQUENCE   546 AA;  58361 MW;  666B6B9C2F2ECD59 CRC64;

  Query Match             34.7%;  Score 42;  DB 1;  Length 546;
  Best Local Similarity   52.9%;  Pred. No. 6.5;
  Matches    9;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;
```

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OM protein - protein search, using sw model

Run on: June 24, 2003, 22:59:44 ; Search time 13 Seconds
(without alignments)
127.619 Million cell updates/sec

Title: US-09-889-331A-47
Perfect score: 121
Sequence: 1 XXXGTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGAXXXXX 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	91	75.2	39	1	EXE3_HELHO	P20394 heloderma h
2	91	75.2	87	1	EXE4_HELSU	P26349 heloderma s
3	42	34.7	546	1	PGMU_ECOLI	P36938 escherichia
4	41	33.9	357	1	YFQB_SCHPO	Q10170 schizosacch
5	41	33.9	589	1	ENC1_HUMAN	O14682 homo sapien
6	41	33.9	589	1	ENC1_MOUSE	O35709 mus musculu
7	41	33.9	2044	1	SIF2_DROME	P91620 drosophila
8	41	33.9	2064	1	SIF1_DROME	P91621 drosophila
9	40	33.1	1017	1	TRL3_HUMAN	Q9hcf6 homo sapien
10	39	32.2	341	1	HRPZ_PSESY	P35674 pseudomonas
11	38	31.4	300	1	TF2B_PYRAB	Q9v0v5 pyrococcus
12	38	31.4	300	1	TF2B_PYRHO	O59151 pyrococcus
13	38	31.4	355	1	NDF1_MESAU	Q60430 mesocricetu
14	38	31.4	357	1	NDF1_MOUSE	Q60867 mus musculu
15	38	31.4	357	1	NDF1_RAT	Q64289 rattus norv
16	38	31.4	419	1	DNLI_ASFM2	P26813 african swi
17	38	31.4	589	1	LU1A_LYCPN	O04973 lycopersico
18	37	30.6	430	1	AST2_YEAST	P39945 saccharomyc
19	37	30.6	488	1	YKT1_CAEEL	P34312 caenorhabdi
20	37	30.6	1237	1	KPB1_RABIT	P18688 oryctolagus
21	36.5	30.2	946	1	K6P2_CANAL	O94200 candida alb
22	36	29.8	318	1	NSR_LACLA	P23648 lactococcus
23	36	29.8	320	1	FEZ2_HUMAN	Q9uhy8 homo sapien
24	36	29.8	324	1	FEZ2_RAT	P97578 rattus norv
25	36	29.8	324	1	GLXA_RHIME	O87389 rhizobium m
26	36	29.8	324	1	VP35_VACCC	P20497 vaccinia vi
27	36	29.8	325	1	VP35_VARV	P33059 variola vir
28	36	29.8	373	1	BIOF_AQUAE	O66875 aquifex aeo
29	36	29.8	401	1	CPXP_BRAJA	Q59203 bradyrhizob
30	36	29.8	413	1	FL1_TOBAC	Q40504 nicotiana t
31	36	29.8	472	1	XYLA_ARATH	Q9fkk7 arabidopsis
32	36	29.8	633	1	SUHR_RHIME	P15715 rhizobium m
33	36	29.8	742	1	SUN2_HUMAN	Q9uh99 homo sapien
34	36	29.8	845	1	SCP1_MESAU	Q60563 mesocricetu
35	36	29.8	1049	1	CARB_SULTO	Q970u7 sulfolobus
36	36	29.8	3068	1	POLG_PEMVC	Q01500 p genome po
37	36	29.8	4473	1	PLE1_CRIGR	Q9ji55 cricetulus
38	36	29.8	4684	1	PLE1_HUMAN	Q15149 homo sapien
39	36	29.8	4687	1	PLE1_RAT	P30427 rattus norv
40	35.5	29.3	111	1	HMGZ_DROME	Q06943 drosophila
41	35	28.9	229	1	COX2_MYXGL	Q9g2x2 myxine glut
42	35	28.9	273	1	FPG_STRMU	P55045 streptococc
43	35	28.9	275	1	FPG_STRPY	Q9a131 streptococc
44	35	28.9	300	1	TF2B_PYRFU	P29095 pyrococcus
45	35	28.9	315	1	T2S1_STRAL	Q53608 streptomyce

ALIGNMENTS

RESULT 1
EXE3_HELHO
ID EXE3_HELHO STANDARD; PRT; 39 AA.
AC P20394;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Exendin-3.
OS Heloderma horridum horridum (Mexican beaded lizard).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Helodermatidae;
OC Heloderma.
OX NCBI_TaxID=8552;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=91056067; PubMed=1700785;
RA Eng J., Andrew P.C., Kleinman W.A., Singh L., Raufman J.-P.;
RT "Purification and structure of exendin-3, a new pancreatic
RT secretagogue isolated from Heloderma horridum venom.";
RL J. Biol. Chem. 265:20259-20262(1990).
CC -!- FUNCTION: HAS A VIP/SECRETIN-LIKE BIOLOGICAL ACTIVITY. INTERACTS
CC WITH THE EXENDIN RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Produced by the venomous gland.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR PIR; A23674; HWGH3Z.
DR HSSP; P01275; 1BH0.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 1.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Toxin; Amidation.
FT MOD_RES 39 39 AMIDATION.
SQ SEQUENCE 39 AA; 4204 MW; A44251D3A4B1D1B9 CRC64;

Query Match 75.2%; Score 91; DB 1; Length 39;
Best Local Similarity 65.6%; Pred. No. 7.6e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| ||||||||    ||||| ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35
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RESULT 2
EXE4_HELSU
ID EXE4_HELSU STANDARD; PRT; 87 AA.
AC P26349;
DT 01-MAY-1992 (Rel. 22, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Exendin-4 precursor.
OS Heloderma suspectum (Gila monster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Helodermatidae;

```
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13707
R;Sone, M.; Hoshino, M.; Suzuki, E.; Kuroda, S.; Kaibuchi, K.; Nakagoshi, H.; Saigo, K.;
Science 275, 543-547, 1997
A;Title: Still life, a protein in synaptic terminals of Drosophila homologous to GDP-GTP
A;Reference number: Z17701; MUID:97153054; PMID:8999801
A;Accession: T13707
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2064 <SON>
A;Cross-references: EMBL:D86547; NID:g1813377; PIDN:BAA13109.1; PID:g1813378
C;Genetics:
A;Cross-references: FlyBase:FBgn0019652

  Query Match             33.9%;  Score 41;  DB 2;  Length 2064;
  Best Local Similarity   41.7%;  Pred. No. 79;
  Matches   10;  Conservative    4;  Mismatches   10;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLKNGGXSSGA 35
              :|   |:||     :|| | |||:
Db       1781 RQIIRESVRNMSIPMKNFGGSSGS 1804


RESULT 13
C69774
transcription regulator phage-related homolog ydcN - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Accession: C69774
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: C69774
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-127 <KUN>
A;Cross-references: GB:Z99106; GB:AL009126; NID:g2632653; PIDN:CAB12289.1; PID:g2632782
A;Experimental source: strain 168
C;Genetics:
A;Gene: ydcN
C;Superfamily: probable transcription repressor yowR

  Query Match             33.1%;  Score 40;  DB 2;  Length 127;
  Best Local Similarity   47.1%;  Pred. No. 6.3;
  Matches    8;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         13 QXEEEAVRLXXXXLKNG 29
              : :||  ||    ||||
Db        100 EFDEETARLVKKALKNG 116


RESULT 14
T45637
beta-D-glucan exohydrolase-like protein - Arabidopsis thaliana
N;Alternate names: protein F13I12.60
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 21-Jul-2000
C;Accession: T45637
R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa
submitted to the Protein Sequence Database, November 1999
A;Reference number: Z23010
A;Accession: T45637
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-609 <CHO>
A;Cross-references: EMBL:AL133292
A;Experimental source: cultivar Columbia; BAC clone F13I12
C;Genetics:
A;Map position: 3
A;Introns: 57/1; 125/2; 155/3; 204/2; 285/3; 320/3; 381/3; 449/1
A;Note: F13I12.60
C;Superfamily: beta-glucosidase

  Query Match             33.1%;  Score 40;  DB 2;  Length 609;
  Best Local Similarity   38.5%;  Pred. No. 33;
  Matches   10;  Conservative    2;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNG 29
              ||      ::   ||||     ||||
Db        376 GTVGCKEHREVAREAVRKSLVLLKNG 401


RESULT 15
T06154
hypothetical protein F24J7.162 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 22-Oct-1999
C;Accession: T06154
R;Bevan, M.; Vitale, D.; Liguori, R.; Argiriou, A.; De Simone, V.; Bancroft, I.; Mewe
submitted to the Protein Sequence Database, April 1999
A;Reference number: Z15493
A;Accession: T06154
A;Molecule type: DNA
A;Residues: 1-772 <BEV>
A;Cross-references: EMBL:AL021768; GSPDB:GN00062; ATSP:F24J7.162
A;Experimental source: cultivar Columbia; BAC clone F24J7
C;Genetics:
A;Gene: ATSP:F24J7.162
A;Map position: 4
A;Introns: 4/2; 42/3; 273/2; 303/2; 342/3; 346/1; 463/3; 485/2; 536/3; 548/3; 576/3;

  Query Match             33.1%;  Score 40;  DB 2;  Length 772;
  Best Local Similarity   37.5%;  Pred. No. 42;
  Matches    9;  Conservative    3;  Mismatches   12;  Indels    0;  Gaps    0;

Qy         11 SKQXEEEAVRLXXXXLKNGGXSSG 34
              | : |||| :     ||:|    |
Db         60 SHKKEEEAKKSSSEGLKDGNAKGG 83


Search completed: June 24, 2003, 23:08:34
Job time : 26 secs
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A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: G90718
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-546 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34142.1; PID:g13360177; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs0719
C;Superfamily: phosphoglucomutase

  Query Match             34.7%;  Score 42;  DB 2;  Length 546;
  Best Local Similarity   52.9%;  Pred. No. 13;
  Matches    9;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLKN 28
              || |:||| :    |||
Db        529 KQIEKEAVEIVSEVLKN 545


RESULT 8
G75266
hypothetical protein DR2500 - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: G75266
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: G75266
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-157 <WHI>
A;Cross-references: GB:AE002079; GB:AE000513; NID:g6460315; PIDN:AAF12045.1; PID:g646032
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR2500
A;Map position: 1
C;Superfamily: Deinococcus radiodurans hypothetical protein DR2500

  Query Match             33.9%;  Score 41;  DB 2;  Length 157;
  Best Local Similarity   42.1%;  Pred. No. 5.1;
  Matches    8;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         16 EEAVRLXXXXLKNGGXSSG 34
              ::||::    ||| |  ||
Db         74 DDAVQVFYRALKNAGLDSG 92


RESULT 9
T38405
hypothetical protein SPAC26A3.17c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C;Accession: T38405; T39165
R;McLean, J.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, February 1996
A;Reference number: Z21791
A;Accession: T38405
A;Molecule type: DNA
A;Residues: 77-357 <MCL>
A;Cross-references: EMBL:Z69240; PIDN:CAA93240.1; GSPDB:GN00066; SPDB:SPAC26A3.17c
A;Experimental source: strain 972h-; cosmid 26A3
R;McLean, J.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, February 1998
A;Reference number: Z21831
A;Accession: T39165
A;Molecule type: DNA
A;Residues: 1-141 <MC2>
A;Cross-references: EMBL:AL021817; PIDN:CAB40198.1; GSPDB:GN00066; SPDB:SPAC8E11.11
A;Experimental source: strain 972h-; cosmid c8E11
C;Genetics:
A;Gene: SPAC8E11.07; SPDB:SPAC26A3.17c; SPDB:SPAC8E11.11
A;Map position: 1

  Query Match             33.9%;  Score 41;  DB 2;  Length 357;
  Best Local Similarity   34.8%;  Pred. No. 12;
  Matches    8;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLKNGGXSSG 34
              |: | :|: :    | |||  :|
Db         64 KETEVQAIEVTKWILSNGGVWNG 86


RESULT 10
A75054
molybdenum cofactor biosynthesis protein (moea-1) PAB1436 - Pyrococcus abyssi (strain
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: A75054
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s
A;Reference number: A75001
A;Accession: A75054
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-402 <KAW>
A;Cross-references: GB:AJ248287; GB:AL096836; NID:g5458657; PIDN:CAB50326.1; PID:g545
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB1436
C;Superfamily: molybdenum cofactor biosynthesis protein moeA-2

  Query Match             33.9%;  Score 41;  DB 2;  Length 402;
  Best Local Similarity   39.1%;  Pred. No. 14;
  Matches    9;  Conservative    4;  Mismatches   10;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLKNGGXSSG 34
              |:  || ||:    : :|| | |
Db        237 KELIEEGVRVADIVVISGGASGG 259


RESULT 11
T13704
still life protein type 2 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13704
R;Sone, M.; Hoshino, M.; Suzuki, E.; Kuroda, S.; Kaibuchi, K.; Nakagoshi, H.; Saigo,
Science 275, 543-547, 1997
A;Title: Still life, a protein in synaptic terminals of Drosophila homologous to GDP-
A;Reference number: Z17701; MUID:97153054; PMID:8999801
A;Accession: T13704
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2044 <SON>
A;Cross-references: EMBL:D86546; NID:g1813375; PIDN:BAA13108.1; PID:g1813376
C;Genetics:
A;Cross-references: FlyBase:FBgn0019652

  Query Match             33.9%;  Score 41;  DB 2;  Length 2044;
  Best Local Similarity   41.7%;  Pred. No. 78;
  Matches   10;  Conservative    4;  Mismatches   10;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLKNGGXSSGA 35
              :|   |:||     :|| | |||:
Db       1761 RQIIRESVRNMSIPMKNFGGSSGS 1784


RESULT 12
T13707
still life protein type 1 - fruit fly (Drosophila melanogaster)
```

```
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35


RESULT 3
D86675
mevalonate kinase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: D86675
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: D86675
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-310 <STO>
A;Cross-references: GB:AE005176; PID:g12723278; PIDN:AAK04502.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: yeaG

  Query Match             34.7%;  Score 42;  DB 2;  Length 310;
  Best Local Similarity   33.3%;  Pred. No. 6.9;
  Matches    7;  Conservative    7;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         13 QXEEEAVRLXXXXLKNGGXSS 33
              : |::|:|:    ||||  ::
Db        285 ENEKDAIRISQRLLKNGAKNT 305


RESULT 4
G64803
phosphoglucomutase (EC 5.4.2.2) - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: G64803; I55076
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G64803
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-546 <BLAT>
A;Cross-references: GB:AE000172; GB:U00096; NID:g1786896; PIDN:AAC73782.1; PID:g1786904;
A;Experimental source: strain K-12, substrain MG1655
R;Lu, M.; Kleckner, N.
J. Bacteriol. 176, 5847-5851, 1994
A;Title: Molecular cloning and characterization of the pgm gene encoding phosphoglucomut
A;Reference number: I55076; MUID:94364967; PMID:8083177
A;Accession: I55076
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-21,'M',23-546 <RES>
A;Cross-references: EMBL:U08369; NID:g473887; PIDN:AAA57067.1; PID:g473888
C;Genetics:
A;Gene: pgm
C;Function:
A;Description: conversion of D-glucose 1-phosphate into D-glucose 6-phosphate; participa
C;Superfamily: phosphoglucomutase
C;Keywords: intramolecular transferase; isomerase; phosphoprotein
F;146/Active site: Ser (phosphoserine intermediate) #status predicted

  Query Match             34.7%;  Score 42;  DB 2;  Length 546;
  Best Local Similarity   52.9%;  Pred. No. 13;
  Matches    9;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLKN 28
              || |:||| :    |||
Db        529 KQIEKEAVEIVSEVLKN 545


RESULT 5
AG0586
phosphoglucomutase [imported] - Salmonella enterica subsp. enterica serovar Typhi (st
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 17-May-2002
C;Accession: AG0586
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se
A;Reference number: AB0502; PMID:11677608
A;Accession: AG0586
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-546 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05161.1; PID:g16501934; GSPDB:GN00176
C;Genetics:
A;Gene: STY0736
C;Superfamily: phosphoglucomutase

  Query Match             34.7%;  Score 42;  DB 2;  Length 546;
  Best Local Similarity   52.9%;  Pred. No. 13;
  Matches    9;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLKN 28
              || |:||| :    |||
Db        529 KQIEKEAVEIVSEVLKN 545


RESULT 6
G85568
phosphoglucomutase [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
C;Accession: G85568
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85568
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-546 <STO>
A;Cross-references: GB:AE005174; NID:g12513593; PIDN:AAG55011.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: pgm
C;Superfamily: phosphoglucomutase

  Query Match             34.7%;  Score 42;  DB 2;  Length 546;
  Best Local Similarity   52.9%;  Pred. No. 13;
  Matches    9;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLKN 28
              || |:||| :    |||
Db        529 KQIEKEAVEIVSEVLKN 545


RESULT 7
G90718
phosphoglucomutase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
C;Accession: G90718
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 24, 2003, 23:03:10 ; Search time 25 Seconds
(without alignments)
153.815 Million cell updates/sec

Title: US-09-889-331A-47
Perfect score: 121
Sequence: 1 XXXGTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGAXXXXX 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	91	75.2	39	1	HWGH3Z	exendin-3 - Mexica
2	91	75.2	39	1	HWGH4G	exendin-4 - Gila m
3	42	34.7	310	2	D86675	mevalonate kinase
4	42	34.7	546	2	G64803	phosphoglucomutase
5	42	34.7	546	2	AG0586	phosphoglucomutase
6	42	34.7	546	2	G85568	phosphoglucomutase
7	42	34.7	546	2	G90718	phosphoglucomutase
8	41	33.9	157	2	G75266	hypothetical prote
9	41	33.9	357	2	T38405	hypothetical prote
10	41	33.9	402	2	A75054	molybdenum cofacto
11	41	33.9	2044	2	T13704	still life protein
12	41	33.9	2064	2	T13707	still life protein
13	40	33.1	127	2	C69774	transcription regu
14	40	33.1	609	2	T45637	beta-D-glucan exoh
15	40	33.1	772	2	T06154	hypothetical prote
16	39	32.2	208	2	D71137	probable transcrip
17	39	32.2	341	2	A40706	extracellular hype
18	39	32.2	688	2	E71845	polyribonucleotide
19	39	32.2	688	2	E64671	polynucleotide pho
20	39	32.2	1649	2	C86822	hypothetical prote
21	38.5	31.8	653	2	T02080	probable carbonate
22	38.5	31.8	1702	2	T14050	protein kinase (EC
23	38	31.4	272	2	AH2847	pyrroline-5-carbox
24	38	31.4	274	2	G97624	delta 1-pyrroline-
25	38	31.4	300	2	E71023	probable transcrip
26	38	31.4	300	2	E75110	transcription init
27	38	31.4	357	2	JC4703	basic helix-loop-h
28	38	31.4	357	2	I49338	neurogenic differe
29	38	31.4	381	2	A57059	beta-cell E-box tr
30	38	31.4	419	2	S23018	DNA ligase (ATP) (
31	38	31.4	421	2	C85644	hypothetical prote
32	38	31.4	421	2	A90784	hypothetical prote
33	38	31.4	636	2	T45640	beta-D-glucan exoh
34	38	31.4	726	2	T20183	hypothetical prote
35	38	31.4	816	2	D96544	unknown protein [i
36	38	31.4	1464	2	T13716	bazooka gene prote
37	37.5	31.0	488	2	C85062	probable thioredox
38	37.5	31.0	608	2	D87912	protein B0205.3 [i
39	37	30.6	157	2	B83897	hypothetical prote
40	37	30.6	189	2	G97690	hypothetical prote
41	37	30.6	189	2	AD2916	transcription regu
42	37	30.6	250	2	AF1095	conserved hypothet
43	37	30.6	250	2	AI1458	conserved hypothet
44	37	30.6	356	2	H90168	GTP-binding protei
45	37	30.6	430	2	S50604	AST2 protein - yea

ALIGNMENTS

RESULT 1
HWGH3Z
exendin-3 - Mexican beaded lizard
C;Species: Heloderma horridum (Mexican beaded lizard)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 21-Nov-1997
C;Accession: A23674
R;Eng, J.; Andrews, P.C.; Kleinman, W.A.; Singh, L.; Raufman, J.P.
J. Biol. Chem. 265, 20259-20262, 1990
A;Title: Purification and structure of exendin-3, a new pancreatic secretagogue isola
A;Reference number: A23674; MUID:91056067; PMID:1700785
A;Accession: A23674
A;Molecule type: protein
A;Residues: 1-39 <ENG>
C;Comment: Exendins are venom components that are thought to bind to receptors for va
g in secretion of amylase.
C;Superfamily: glucagon
C;Keywords: amidated carboxyl end; duplication; secretagogue; venom
F;39/Modified site: amidated carboxyl end (Ser) #status experimental

Query Match 75.2%; Score 91; DB 1; Length 39;
Best Local Similarity 65.6%; Pred. No. 7.7e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||| ||||
Db          4 GTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGA 35
```

RESULT 2
HWGH4G
exendin-4 - Gila monster
C;Species: Heloderma suspectum (Gila monster)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 21-Nov-1997
C;Accession: A42486
R;Eng, J.; Kleinman, W.A.; Singh, L.; Singh, G.; Raufman, J.P.
J. Biol. Chem. 267, 7402-7405, 1992
A;Title: Isolation and characterization of exendin-4, an exendin-3 analogue, from Hel
A;Reference number: A42486; MUID:92218391; PMID:1313797
A;Accession: A42486
A;Molecule type: protein
A;Residues: 1-39 <ENG>
C;Comment: Exendin-4 does not stimulate amylase secretion by pancreatic acinar cells.
C;Superfamily: glucagon
C;Keywords: amidated carboxyl end; duplication; venom
F;39/Modified site: amidated carboxyl end (Ser) #status experimental

Query Match 75.2%; Score 91; DB 1; Length 39;
Best Local Similarity 65.6%; Pred. No. 7.7e-10;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
              ||     ||| |||||||    ||||| ||||
```

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB001488; BAA19320.1; -.
DR EMBL; Z99106; CAB12289.1; -.
DR InterPro; IPR001387; HTH_3.
DR Pfam; PF01381; HTH_3; 1.
DR SMART; SM00530; HTH_XRE; 1.
KW Complete proteome.
SQ SEQUENCE 127 AA; 14649 MW; 3CC91D5B1D51628C CRC64;

Query Match 33.1%; Score 40; DB 16; Length 127;
Best Local Similarity 47.1%; Pred. No. 12;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

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Qy         13 QXEEEAVRLXXXXLKNG 29
              : :||  ||    ||||
Db        100 EFDEETARLVKKALKNG 116
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Search completed: June 24, 2003, 23:07:38
Job time : 52.5 secs

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RL   Science 287:2185-2195(2000).
DR   EMBL; AE003565; AAF50756.2; -.
DR   HSSP; P08567; 1PLS.
DR   FlyBase; FBgn0019652; sif.
DR   InterPro; IPR001331; GDS_CDC24.
DR   InterPro; IPR001478; PDZ.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR003116; RBD.
DR   InterPro; IPR000219; RhoGEF.
DR   Pfam; PF00169; PH; 2.
DR   Pfam; PF02196; RBD; 1.
DR   Pfam; PF00621; RhoGEF; 1.
DR   SMART; SM00228; PDZ; 1.
DR   SMART; SM00233; PH; 2.
DR   SMART; SM00455; RBD; 1.
DR   SMART; SM00325; RhoGEF; 1.
DR   PROSITE; PS00741; DH_1; UNKNOWN_1.
DR   PROSITE; PS50106; PDZ; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
SQ   SEQUENCE   2044 AA;  228329 MW;  1ACDFBEA63E3FBC1 CRC64;

  Query Match             33.9%;  Score 41;  DB 5;  Length 2044;
  Best Local Similarity   41.7%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    4;  Mismatches   10;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLKNGGXSSGA 35
              :|   |:||     :|| | |||:
Db       1761 RQIIRESVRNMSIPMKNFGGSSGS 1784


RESULT 14
Q9VRN7
ID   Q9VRN7      PRELIMINARY;      PRT;  2045 AA.
AC   Q9VRN7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Sif protein.
GN   SIF OR CG5256 OR CG5406.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AE003565; AAF50755.2; -.
DR   HSSP; P08567; 1PLS.
DR   FlyBase; FBgn0019652; sif.
DR   InterPro; IPR001331; GDS_CDC24.
DR   InterPro; IPR001478; PDZ.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR003116; RBD.
DR   InterPro; IPR000219; RhoGEF.
DR   InterPro; IPR001960; WH1.
DR   Pfam; PF00169; PH; 2.
DR   Pfam; PF02196; RBD; 1.
DR   Pfam; PF00621; RhoGEF; 1.
DR   SMART; SM00228; PDZ; 1.
DR   SMART; SM00233; PH; 2.
DR   SMART; SM00455; RBD; 1.
DR   SMART; SM00325; RhoGEF; 1.
DR   SMART; SM00461; WH1; 1.
DR   PROSITE; PS00741; DH_1; UNKNOWN_1.
DR   PROSITE; PS50106; PDZ; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
SQ   SEQUENCE   2045 AA;  228386 MW;  A34956429EA3603B CRC64;

  Query Match             33.9%;  Score 41;  DB 5;  Length 2045;
  Best Local Similarity   41.7%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    4;  Mismatches   10;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLKNGGXSSGA 35
              :|   |:||     :|| | |||:
Db       1762 RQIIRESVRNMSIPMKNFGGSSGS 1785


RESULT 15
P96631
ID   P96631      PRELIMINARY;      PRT;  127 AA.
AC   P96631;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Probable repressor protein.
GN   YDCN.
OS   Bacillus subtilis.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC   Bacillaceae; Bacillus.
OX   NCBI_TaxID=1423;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RX   MEDLINE=98000887; PubMed=9341680;
RA   Beloin C., Ayora S., Exley R., Hirschbein L., Ogasawara N.,
RA   Kasahara Y., Alonso J.C., Le Hegarat F.;
RT   "Characterization of an lrp-like (lrpC) gene from Bacillus subtilis.";
RL   Mol. Gen. Genet. 256:63-71(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RX   MEDLINE=98044033; PubMed=9384377;
RA   Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA   Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA   Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA   Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
```

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KW   Coat protein.
SQ   SEQUENCE   306 AA;  33890 MW;  4456EBB53E174298 CRC64;

  Query Match             33.9%;  Score 41;  DB 12;  Length 306;
  Best Local Similarity   43.5%;  Pred. No. 20;
  Matches   10;  Conservative    1;  Mismatches   12;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLKNGGXSSG 34
              |  |  :  |    |||||  ||
Db         62 KLKEFNSQNLTAGELKNGGFESG 84


RESULT 11
Q9UYT6
ID   Q9UYT6      PRELIMINARY;      PRT;   402 AA.
AC   Q9UYT6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Molybdenum cofactor biosynthesis protein (MOEA-1).
GN   PAB1436.
OS   Pyrococcus abyssi.
OC   Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC   Pyrococcus.
OX   NCBI_TaxID=29292;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ORSAY;
RA   Heilig R.;
RT   "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
RT   structure and evolution.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ248287; CAB50326.1; -.
DR   InterPro; IPR002106; AAtRNA_ligaseII.
DR   InterPro; IPR001453; MoCF_biosynth.
DR   InterPro; IPR005111; MoeA_C.
DR   InterPro; IPR005110; MoeA_N.
DR   Pfam; PF00994; MoCF_biosynth; 1.
DR   Pfam; PF03454; MoeA_C; 1.
DR   Pfam; PF03453; MoeA_N; 1.
DR   ProDom; PD002460; MoCF_biosynth; 1.
DR   TIGRFAMs; TIGR00177; molyb_syn; 1.
DR   PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
KW   Complete proteome.
SQ   SEQUENCE   402 AA;  43327 MW;  44545EDA70F6A78E CRC64;

  Query Match             33.9%;  Score 41;  DB 17;  Length 402;
  Best Local Similarity   39.1%;  Pred. No. 27;
  Matches    9;  Conservative    4;  Mismatches   10;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLKNGGXSSG 34
              |:  || ||:    : :|| | |
Db        237 KELIEEGVRVADIVVISGGASGG 259


RESULT 12
Q96L69
ID   Q96L69      PRELIMINARY;      PRT;   589 AA.
AC   Q96L69;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Ectodermal-neural cortex.
GN   ENC1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Feng Z., Zhang B., Peng X., Yuan J., Qiang B.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY049781; AAL15438.1; -.
DR   InterPro; IPR000210; BTB_POZ.
DR   InterPro; IPR001798; Kelch.
DR   InterPro; IPR000169; SHprot_acsite.
DR   Pfam; PF00651; BTB; 1.
DR   Pfam; PF01344; Kelch; 5.
DR   PROSITE; PS50097; BTB; 1.
DR   PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
SQ   SEQUENCE   589 AA;  66113 MW;  E5CB1466DB8CA16E CRC64;

  Query Match             33.9%;  Score 41;  DB 4;  Length 589;
  Best Local Similarity   45.0%;  Pred. No. 41;
  Matches    9;  Conservative    3;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         11 SKQXEEEAVRLXXXXLKNGG 30
              ||:  |||:|    |:| |
Db        262 SKEIVEEAIRCKLKILQNDG 281


RESULT 13
Q9VRN8
ID   Q9VRN8      PRELIMINARY;      PRT;  2044 AA.
AC   Q9VRN8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Sif protein.
GN   SIF OR CG5256 OR CG5406.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
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DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Putative deaminase.
GN   2SCK31.34 OR SCO4974.
OS   Streptomyces coelicolor.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1902;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RA   Oliver K., Harris D.;
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RA   Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RX   MEDLINE=97000351; PubMed=8843436;
RA   Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
RA   Kinashi H., Hopwood D.A.;
RT   "A set of ordered cosmids and a detailed genetic and physical map for
RT   the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL   Mol. Microbiol. 21:77-96(1996).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2) / M145;
RA   Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA   Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA   Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA   Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA   Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA   Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA   Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA   Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA   Hopwood D.A.;
RT   "Complete genome sequence of the model actinomycete Streptomyces
RT   coelicolor A3(2).";
RL   Nature 417:141-147(2002).
DR   EMBL; AL451182; CAC18715.2; -.
DR   EMBL; AL512667; CAD30959.1; -.
DR   InterPro; IPR002125; dCMP/cyt_deam.
DR   Pfam; PF00383; dCMP_cyt_deam; 1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   167 AA;  18334 MW;  3D2044BA11F6E9B1 CRC64;

  Query Match             33.9%;  Score 41;  DB 16;  Length 167;
  Best Local Similarity   35.0%;  Pred. No. 10;
  Matches    7;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         16 EEAVRLXXXXLKNGGXSSGA 35
              ::|: |    ::|||   ||
Db         19 DKAIELATTSVRNGGGPFGA 38


RESULT 9
O42143
ID   O42143      PRELIMINARY;      PRT;   266 AA.
AC   O42143;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Glucagon I precursor [Contains: Glucagon; glucagon-like peptide 1A
DE   (GLP-1A); glucagon-like peptide 1B (GLP-1B); glucagon-like peptide 1C
DE   (GLP-1C); glucagon-like peptide 2 (GLP-2)].
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC   TISSUE=PANCREAS;
RX   MEDLINE=97368292; PubMed=9223287;
RA   Irwin D.M., Satkunarajah M., Wen Y., Brubaker P.L., Pederson R.A.,
RA   Wheeler M.B.;
RT   "The Xenopus proglucagon gene encodes novel GLP-1-like peptides with
RT   insulinotropic properties.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:7915-7920(1997).
CC   -!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
CC       THE BLOOD SUGAR LEVEL.
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
CC       PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR   EMBL; AF004432; AAB65660.1; -.
DR   HSSP; P01274; 1GCN.
DR   InterPro; IPR000532; Glucagon.
DR   Pfam; PF00123; hormone2; 5.
DR   PRINTS; PR00275; GLUCAGON.
DR   SMART; SM00070; GLUCA; 5.
DR   PROSITE; PS00260; GLUCAGON; 5.
KW   Glucagon family; Hormone; Signal; Cleavage on pair of basic residues;
KW   Multigene family; Alternative splicing.
FT   SIGNAL       1      ?       POTENTIAL.
FT   PEPTIDE     53     81       GLUCAGON.
FT   PEPTIDE     97    133       GLUCAGON-LIKE PEPTIDE 1A.
FT   PEPTIDE    142    173       GLUCAGON-LIKE PEPTIDE 1B.
FT   PEPTIDE    180    211       GLUCAGON-LIKE PEPTIDE 1C.
FT   PEPTIDE    227    259       GLUCAGON-LIKE PEPTIDE 2.
FT   VARSPLIC   214    261       MISSING (IN ISOFORM 2).
SQ   SEQUENCE   266 AA;  30951 MW;  544F7BBC20AF872C CRC64;

  Query Match             33.9%;  Score 41;  DB 13;  Length 266;
  Best Local Similarity   34.5%;  Pred. No. 17;
  Matches   10;  Conservative    5;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXS 32
              ||     ::| :|:| :     | ||| |
Db        100 GTFTSDVTQQLDEKAAKEFIDWLINGGPS 128


RESULT 10
O92527
ID   O92527      PRELIMINARY;      PRT;   306 AA.
AC   O92527;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Coat protein (Capsid protein).
OS   Carnation latent virus (CLV).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
OX   NCBI_TaxID=12164;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Meehan B.M.;
RL   Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91324119; PubMed=1713905;
RA   Meehan B.M., Mills P.R.;
RT   "Nucleotide sequence of the 3'-terminal region of carnation latent
RT   virus.";
RL   Intervirology 32:262-267(1991).
CC   -!- FUNCTION: SELF-ASSEMBLES WITH THE RNA TO FORM INFECTIOUS PARTICLES
CC       (BY SIMILARITY).
CC   -!- SIMILARITY: TO THE COAT PROTEINS OF OTHER POTEXVIRUSES.
DR   EMBL; AJ010697; CAA09306.1; -.
DR   InterPro; IPR000052; Pltvir_coat.
DR   Pfam; PF00286; virus_P-coat; 1.
DR   PRINTS; PR00232; POTXCARLCOAT.
DR   ProDom; PD000603; Pltvir_coat; 1.
DR   PROSITE; PS00418; POTEX_CARLAVIRUS_COAT; 1.
```

```
AC   Q8Z8F1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Phosphoglucomutase.
GN   STY0736.
OS   Salmonella typhi.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Salmonella.
OX   NCBI_TaxID=601;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CT18;
RX   MEDLINE=21534947; PubMed=11677608;
RA   Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA   Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA   Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA   Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA   Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA   Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA   Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA   Whitehead S., Barrell B.G.;
RT   "Complete genome sequence of a multiple drug resistant Salmonella
RT   enterica serovar Typhi CT18.";
RL   Nature 413:848-852(2001).
DR   EMBL; AL627267; CAD05161.1; -.
DR   InterPro; IPR001485; PG/PMM_mutase.
DR   Pfam; PF00408; PGM_PMM; 1.
DR   Pfam; PF02878; PGM_PMM_I; 1.
DR   Pfam; PF02879; PGM_PMM_II; 1.
DR   Pfam; PF02880; PGM_PMM_III; 1.
DR   TIGRFAMs; TIGR01132; pgm; 1.
DR   PROSITE; PS00710; PGM_PMM; 1.
KW   Complete proteome.
SQ   SEQUENCE   546 AA;  58127 MW;  6F73775E0B886CD8 CRC64;

  Query Match             34.7%;  Score 42;  DB 16;  Length 546;
  Best Local Similarity   52.9%;  Pred. No. 24;
  Matches    9;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLKN 28
              || |:||| :    |||
Db        529 KQIEKEAVEIVSEVLKN 545


RESULT 6
Q8X9G6
ID   Q8X9G6      PRELIMINARY;      PRT;   546 AA.
AC   Q8X9G6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Phosphoglucomutase.
GN   PGM OR Z0837 OR ECS0719.
OS   Escherichia coli O157:H7.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=83334;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX   MEDLINE=21074935; PubMed=11206551;
RA   Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA   Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA   Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA   Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA   Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA   Welch R.A., Blattner F.R.;
RT   "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL   Nature 409:529-533(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / RIMD 0509952;
RX   MEDLINE=21156231; PubMed=11258796;
RA   Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA   Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA   Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA   Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT   "Complete genome sequence of enterohemorrhagic Escherichia coli
RT   O157:H7 and genomic comparison with a laboratory strain K-12.";
RL   DNA Res. 8:11-22(2001).
DR   EMBL; AE005247; AAG55011.1; -.
DR   EMBL; AP002552; BAB34142.1; -.
DR   InterPro; IPR001485; PG/PMM_mutase.
DR   Pfam; PF00408; PGM_PMM; 1.
DR   Pfam; PF02878; PGM_PMM_I; 1.
DR   Pfam; PF02879; PGM_PMM_II; 1.
DR   Pfam; PF02880; PGM_PMM_III; 1.
DR   PROSITE; PS00710; PGM_PMM; 1.
KW   Complete proteome.
SQ   SEQUENCE   546 AA;  58335 MW;  0605228081D7A31B CRC64;

  Query Match             34.7%;  Score 42;  DB 16;  Length 546;
  Best Local Similarity   52.9%;  Pred. No. 24;
  Matches    9;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         12 KQXEEEAVRLXXXXLKN 28
              || |:||| :    |||
Db        529 KQIEKEAVEIVSEVLKN 545


RESULT 7
Q9RRJ0
ID   Q9RRJ0      PRELIMINARY;      PRT;   157 AA.
AC   Q9RRJ0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Hypothetical protein DR2500.
GN   DR2500.
OS   Deinococcus radiodurans.
OC   Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OC   Deinococcaceae; Deinococcus.
OX   NCBI_TaxID=1299;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=R1;
RX   MEDLINE=20036896; PubMed=10567266;
RA   White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA   Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA   Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA   Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA   Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA   Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA   Fraser C.M.;
RT   "Genome sequence of the radioresistant bacterium Deinococcus
RT   radiodurans R1.";
RL   Science 286:1571-1577(1999).
DR   EMBL; AE002079; AAF12045.1; -.
DR   TIGR; DR2500; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   157 AA;  17027 MW;  B766BD89F60A5B5D CRC64;

  Query Match             33.9%;  Score 41;  DB 16;  Length 157;
  Best Local Similarity   42.1%;  Pred. No. 9.6;
  Matches    8;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         16 EEAVRLXXXXLKNGGXSSG 34
              ::||::    ||| |  ||
Db         74 DDAVQVFYRALKNAGLDSG 92


RESULT 8
Q9ADJ9
ID   Q9ADJ9      PRELIMINARY;      PRT;   167 AA.
AC   Q9ADJ9;
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=> d his

     (FILE 'HOME' ENTERED AT 08:20:10 ON 25 JUN 2003)
           SET COST OFF

     FILE 'REGISTRY' ENTERED AT 08:20:19 ON 25 JUN 2003
L1          464 S [HRY][SGAT][DE]GT.[TS][TS][DE].SKQ.EEEAVRL..[ED].LKNGG.SSGA..
           SAV L1 LIU889/A

     FILE 'HCAPLUS' ENTERED AT 08:25:49 ON 25 JUN 2003
L2           52 S L1
           E YOUNG A/AU
L3          108 S E3,E4
           E YOUNG ANDREW/AU
L4          101 S E3,E4
L5            2 S E20
           E BRONISLAVA G/AU
           E GEDULIN/AU
L6           21 S E4,E7,E8
L7            7 S L2 AND L3-L6
           E AMYLIN/PA,CS
L8            8 S E3-E25 AND L2
L9            9 S L7,L8
L10          25 S L2 AND (PD<=19990114 OR PRD<=19990114 OR AD<=19990114)
L11           6 S L10 AND L9
L12           9 S L9,L11
L13          19 S L10 NOT L12
L14           9 S L13 AND P/DT
L15          10 S L13 NOT L14

=> d que l1
L1          464 SEA FILE=REGISTRY ABB=ON  PLU=ON  [HRY][SGAT][DE]GT.[TS][TS][DE
           ].SKQ.EEEAVRL..[ED].LKNGG.SSGA...[STY]|.[SGAT][DE]GT.[TS][TS][D
           E].SKQ.EEEAVRL..[ED].L/SQSP


=> fil hcaplus
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FILE LAST UPDATED: 24 Jun 2003  (20030624/ED)

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 substance identification.


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L12  ANSWER 1 OF 9  HCAPLUS  COPYRIGHT 2003 ACS
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jan.delaval@uspto.gov

AN 2003:355827 HCAPLUS
DN 138:374157
TI Novel exendin agonist formulations and methods of administration thereof
IN **Young, Andrew A.**; Kolterman, Orville G.
PA USA
SO U.S. Pat. Appl. Publ., 104 pp., Cont.-in-part of U.S. Ser. No. 889,330.
CODEN: USXXCO
DT Patent
LA English
FAN.CNT 4

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 2003087820	A1	20030508	US 2002-157224	20020528 <--
WO 2000041546	A2	20000720	WO 2000-US902	20000114 <--

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI US 1999-116380P	P	19990114 <--	
US 2000-175365P	P	20000110	
WO 2000-US902	W	20000114	
US 2001-889330	A2	20011227	

AB Novel exendin and exendin agonist compd. formulations and dosages and methods of administration thereof are provided. These compns. and methods are useful in treating diabetes and conditions that would be benefited by lowering plasma glucose or delaying and/or slowing gastric emptying or inhibiting food intake.

IT **522007-52-9 522007-56-3 522007-58-5**
522007-60-9
RL: PRP (Properties)
(Unclaimed; novel exendin agonist formulations and methods of administration thereof)

IT **521986-08-3**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(unclaimed protein sequence; exendin agonist formulations and methods of administration thereof)

IT **522007-04-1 522007-08-5 522007-09-6**
522007-10-9 522007-11-0 522007-12-1
522007-13-2 522007-14-3 522007-15-4
522007-16-5 522007-17-6 522007-18-7
522007-19-8 522007-20-1 522007-21-2
522007-22-3 522007-23-4 522007-24-5
522007-25-6 522007-26-7 522007-27-8
522007-28-9 522007-29-0 522007-30-3
522007-31-4 522007-32-5 522007-33-6
522007-34-7 522007-35-8 522007-36-9
522007-37-0 522007-38-1 522007-39-2
522007-40-5 522007-41-6 522007-42-7
522007-43-8 522007-44-9 522007-45-0
522007-46-1 522007-47-2 522007-48-3
522007-49-4 522007-50-7 522007-51-8
522007-53-0 522007-54-1 522007-55-2
522007-57-4 522007-59-6 522007-61-0
522007-62-1 522007-63-2 522007-64-3
522007-65-4 522007-66-5 522007-70-1
522007-71-2 522007-78-9 522007-80-3
RL: PRP (Properties)

(unclaimed protein sequence; novel exendin agonist formulations and methods of administration thereof)

IT **165338-05-6**, 1-31-Exendin 4 (Heloderma suspectum)
210712-28-0, 1-30-Exendin 4 (Heloderma suspectum)
238091-56-0 238091-57-1 238091-58-2
238091-60-6 238091-62-8 238091-66-2
238091-74-2 238091-76-4 238091-77-5
238091-78-6 238091-79-7 238091-80-0
238091-81-1 238091-82-2 238091-83-3
238091-84-4 238091-86-6 238091-87-7
238091-92-4 238091-93-5 238091-94-6
351208-37-2 351208-40-7 351208-44-1
351208-45-2 351208-46-3 351208-47-4
351208-48-5 351208-53-2 351208-54-3 35120
8-59-8 351208-60-1 351208-61-2
351208-62-3 351208-72-5 351208-74-7
351208-93-0 351208-94-1 351208-97-4
351208-98-5 351208-99-6 351209-00-2
351209-03-5 351209-04-6 351209-05-7
351209-06-8 351209-07-9 351209-11-5
521913-27-9
RL: PRP (Properties)
(unclaimed sequence; novel exendin agonist formulations and methods of administration thereof)

L12 ANSWER 2 OF 9 HCAPLUS COPYRIGHT 2003 ACS
AN 2001:525943 HCAPLUS
DN 135:132445
TI Use of exendins and agonists thereof for modulation of triglyceride levels and treatment of dyslipidemia
IN Kolterman, Orville Gene; **Young, Andrew A.**
PA **Amylin Pharmaceuticals, Inc., USA**
SO PCT Int. Appl., 161 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 4

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001051078	A1	20010719	WO 2001-US719	20010109
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	EP 1246638	A1	20021009	EP 2001-900978	20010109
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
	US 2003036504	A1	20030220	US 2001-756690	20010109
	JP 2003519667	T2	20030624	JP 2001-551501	20010109
PRAI	US 2000-175365P	P	20000110		
	WO 2001-US719	W	20010109		

AB Methods for modulating the levels of plasma triglyceride and other lipids in a subject comprise administration of an effective amt. of an exendin or exendin agonist, alone or in conjunction with other compds. or compns. that lower blood triglyceride and/or other lipid levels.

IT **210712-29-1 210712-30-4 210712-33-7**
210712-34-8 210712-36-0 210712-38-2
210712-42-8 210712-50-8 210712-52-0

210712-53-1 210712-69-9
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(exendins and agonists for modulation of triglyceride levels and treatment of dyslipidemia)

IT **203743-40-2 238410-89-4 238410-90-7**
238411-00-2 238411-01-3 238411-02-4
238411-03-5 238411-04-6 238411-05-7
238411-06-8 238411-07-9 238411-08-0
238411-10-4 238748-48-6 306277-48-5
351350-30-6 351350-32-8 351350-38-4
351350-40-8 351350-43-1 351350-44-2
351350-45-3 351350-47-5 351350-91-9
351351-05-8 351351-08-1 351351-09-2
351351-14-9 351351-29-6 351351-46-7
351351-47-8 351376-16-4 351376-17-5
351376-18-6 351376-19-7 351376-20-0
351376-22-2 351376-23-3 351376-24-4
351376-25-5 351376-49-3
RL: PRP (Properties)
(unclaimed protein sequence; use of exendins and agonists thereof for modulation of triglyceride levels and treatment of dyslipidemia)

IT **165338-05-6**, 1-31-Exendin 4 (Heloderma suspectum)
210712-28-0, 1-30-Exendin 4 (Heloderma suspectum)
238091-60-6 238091-78-6 238091-79-7
238091-80-0 238091-81-1 238091-82-2
238091-83-3 238091-84-4 238091-86-6
238091-87-7 238091-92-4 238091-93-5
238091-94-6 351208-37-2 351208-38-3
351208-39-4 351208-40-7 351208-44-1
351208-45-2 351208-46-3 351208-47-4
351208-48-5 351208-51-0 351208-52-1
351208-53-2 351208-54-3 351208-59-8
351208-60-1 351208-61-2 351208-62-3
351208-63-4 351208-64-5 351208-72-5
351208-74-7 351208-75-8 351208-77-0
351208-91-8 351208-92-9 351208-93-0
351208-94-1 351208-95-2 351208-96-3
351208-97-4 351208-98-5 351208-99-6
351209-00-2 351209-03-5 351209-04-6
351209-05-7 351209-06-8 351209-07-9
351209-11-5 351351-15-0
RL: PRP (Properties)
(unclaimed sequence; use of exendins and agonists thereof for modulation of triglyceride levels and treatment of dyslipidemia)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Amylin Pharmaceuticals	1998			WO 9830231 A	HCAPLUS
Amylin Pharmaceuticals	2000			WO 0066629 A	HCAPLUS
Andersson, K	1999			WO 9962872 A	HCAPLUS
Kolterman, O	2000	43	A189	DIABETOLOGIA, 36th A	
Ligand Pharm Inc	1998			WO 9805331 A	HCAPLUS
Warner Lambert Co	1999			WO 9930706 A	HCAPLUS
Young, A	1999	48	1026	DIABETES	HCAPLUS

L12 ANSWER 3 OF 9 HCAPLUS COPYRIGHT 2003 ACS
AN 2000:861704 HCAPLUS
DN 134:37033
TI Use of exendins and agonists thereof for the treatment of gestational diabetes mellitus

IN Hiles, Richard; Prickett, Kathryn S.
PA **Amylin Pharmaceuticals, Inc., USA**
SO PCT Int. Appl., 133 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000073331	A2	20001207	WO 2000-US14231	20000523
	WO 2000073331	A3	20010628		
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	US 6506724	B1	20030114	US 1999-323867	19990601
	EP 1181043	A2	20020227	EP 2000-937710	20000523
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
	JP 2003501361	T2	20030114	JP 2001-500655	20000523
PRAI	US 1999-323867	A	19990601		
	WO 2000-US14231	W	20000523		

AB Methods for treating gestational diabetes which comprise administration of an effective amt. of an exendin or an exendin agonist, alone or in conjunction with other compds. or compns. that lower blood glucose levels.

IT **210829-08-6P**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(use of exendins and agonists thereof for treatment of gestational diabetes mellitus in relation to combination with insulin or amyhclin agonist)

IT **158345-16-5P 203743-29-7P 203743-31-1P**
203743-32-2P 203743-33-3P 203743-35-5P
203743-36-6P 203743-37-7P 203743-38-8P
203743-41-3P 203743-45-7P 203743-46-8P
203743-47-9P 203743-50-4P 210712-28-0P,
1-30-Exendin 4 (Heloderma suspectum) **210712-29-1P**
210712-30-4P 210712-31-5P 210712-33-7P
210712-34-8P 210712-36-0P 210712-38-2P
210712-42-8P 210712-50-8P 210712-52-0P
210712-53-1P 210712-54-2P 210712-55-3P
210712-56-4P 210712-57-5P 210712-58-6P
210712-59-7P 210712-60-0P 210712-61-1P
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210830-59-4P 238091-49-1P 238091-55-9P
284676-24-0P 312925-06-7P 312925-07-8P
312925-08-9P 312925-09-0P 312925-10-3P
312932-20-0P 312932-28-8P 312932-49-3P
312932-83-5P 312933-83-8P 312949-21-6P
312949-26-1P
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(use of exendins and agonists thereof for treatment of gestational diabetes mellitus in relation to combination with insulin or amylin agonist)

IT **130357-25-4**, Exendin 3 (Heloderma horridum) **141758-74-9**, Exendin 4 (Heloderma suspectum) **203743-40-2**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(use of exendins and agonists thereof for treatment of gestational diabetes mellitus in relation to combination with insulin or amylin agonist)

L12 ANSWER 4 OF 9 HCAPLUS COPYRIGHT 2003 ACS
AN 2000:790546 HCAPLUS
DN 133:359242
TI Modified exendins and exendin agonists
IN **Young, Andrew**; Prickett, Kathryn
PA **Amylin Pharmaceuticals, Inc., USA**
SO PCT Int. Appl., 119 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000066629	A1	20001109	WO 2000-US11814	20000428
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	EP 1175443	A1	20020130	EP 2000-928685	20000428
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
	BR 2000010705	A	20020205	BR 2000-10705	20000428
	JP 2002544127	T2	20021224	JP 2000-615657	20000428
PRAI	US 1999-132018P	P	19990430		
	WO 2000-US11814	W	20000428		

AB Novel modified exendins and exendin agonists having an exendin or exendin agonist linked to one or more polyethylene glycol polymers, for example, and related formulations and dosages and methods of administration thereof are provided. These modified exendins and exendin agonists, compns. and methods are useful in treating diabetes and conditions that would be benefited by lowering plasma glucose or delaying and/or slowing gastric emptying or inhibiting food intake.

IT **210712-29-1 210712-30-4 210712-31-5**
210712-33-7 210712-34-8 210712-38-2
210712-42-8 210712-50-8 210712-52-0
210712-53-1 210712-54-2 210712-55-3
210712-56-4 210712-57-5 210712-58-6
210712-59-7 210712-61-1 210712-62-2
210712-64-4 210712-65-5 210712-67-7
210712-68-8 210712-69-9 210712-73-5
210712-77-9 210712-79-1 210712-80-4
210712-81-5 210712-84-8 210712-85-9
210712-90-6 210712-91-7 210712-92-8
210712-93-9 210712-94-0 210712-95-1
210713-02-3 210713-03-4 210713-04-5
210713-05-6 210713-18-1 210713-19-2
210713-20-5 210713-21-6 210713-22-7
210713-28-3 210713-29-4 210713-30-7
210713-31-8 210713-33-0 210713-38-5
210824-14-9 210824-35-4 210824-60-5
210824-78-5 210824-96-7 210828-38-9
210828-61-8 210828-91-4 210829-01-9
210829-03-1 210829-08-6 210829-11-1
210829-12-2 210829-35-9 210829-36-0
210829-38-2 210829-43-9 210829-57-5
210829-60-0 210829-61-1 238091-55-9
239091-09-9 307499-16-7 307499-17-8
307499-18-9 307499-38-3 307499-42-9
307499-43-0 307499-44-1 307499-45-2
307499-46-3 307499-47-4 307499-48-5
307499-60-1 307499-61-2 307499-62-3
307499-63-4 307499-64-5 307499-65-6
307499-66-7 307499-67-8 307518-01-0
307518-02-1 307519-08-0
RL: PRP (Properties)
(Unclaimed; modified exendins and exendin agonists)

IT **305814-59-9P 305814-98-6P 305815-14-9P**
305815-15-0P 305815-18-3P 305815-27-4P
305815-28-5P 305815-30-9P 305818-24-0P
305818-90-0P
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PNU (Preparation, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(modified exendins and exendin agonists)

IT **130357-25-4,** Exendin 3 (Heloderma horridum) **141758-74-9,**
Exendin 4 (Heloderma suspectum)
RL: PRP (Properties)
(unclaimed sequence; modified exendins and exendin agonists)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Katre, N	1988			US 4766106 A	HCAPLUS
Kjeld, M	1999			WO 9943708 A	HCAPLUS
Meurer, J	1999	48	716	Metabolism Clinical	HCAPLUS
Novonordisk, A	1998			WO 9808871 A	HCAPLUS
Young, A	1998			WO 9805351 A	HCAPLUS
Zalipsky, S	1992			US 5122614 A	HCAPLUS

L12 ANSWER 5 OF 9 HCAPLUS COPYRIGHT 2003 ACS
AN 2000:493318 HCAPLUS
DN 133:129880
TI Methods using an exendin or related substance for glucagon suppression
IN **Young, Andrew; Gedulin, Bronislava**

PA **Amylin Pharmaceuticals, Inc., USA**
SO PCT Int. Appl., 96 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 4

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	WO 2000041548	A2	20000720	WO 2000-US942	20000114	<--
	WO 2000041548	A3	20001130			
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM					
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG					
	CA 2356331	AA	20000720	CA 2000-2356331	20000114	<--
	EP 1143989	A2	20011017	EP 2000-902415	20000114	<--
	EP 1143989	A3	20020911			
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO					
	BR 2000007823	A	20011120	BR 2000-7823	20000114	<--
	JP 2002538084	T2	20021112	JP 2000-593169	20000114	<--
	NO 2001003469	A	20010914	NO 2001-3469	20010712	<--
PRAI	US 1999-116380P	P	19990114	<--		
	US 1999-132017P	P	19990430			
	US 2000-175365P	P	20000110			
	WO 2000-US942	W	20000114			

AB Methods are provided for use of an exendin, an exendin agonist, or a modified exendin or exendin agonist having an exendin or exendin agonist linked to one or more polyethylene glycol polymers, for example, for lowering glucagon levels and/or suppressing glucagon secretion in a subject. These methods are useful in treating hyperglucagonemia and other conditions that would be benefited by lowering plasma glucagon or suppressing glucagon secretion.

IT **130357-25-4P**, Exendin 3 (Heloderma horridum) **141758-74-9P**
, Exendin 4 (Heloderma suspectum)
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(exendin or related substance for glucagon suppression)

IT **141758-74-9**, Exendin 4 (Heloderma suspectum) **284676-24-0**
286009-44-7 286009-59-4 286369-29-7
286369-42-4 286369-43-5
RL: PRP (Properties)
(unclaimed protein sequence; methods using an exendin or related substance for glucagon suppression)

IT **210712-28-0**, 1-30-Exendin 4 (Heloderma suspectum)
210712-29-1 210712-30-4 210712-31-5
210712-33-7 210712-34-8 210712-38-2
210712-42-8 210712-50-8 210712-52-0
210712-53-1 210712-54-2 210712-55-3
210712-56-4 210712-57-5 210712-58-6
210712-59-7 210712-60-0 210712-61-1
210712-62-2 210712-69-9 210712-73-5
210712-77-9 210712-78-0 210712-79-1
210712-80-4 210712-81-5 210712-84-8
210712-91-7 210712-92-8 210713-02-3
210713-03-4 210713-18-1 210713-19-2

210713-22-7 210713-23-8 210713-24-9
210713-25-0 210713-28-3 210713-29-4
210713-31-8 210713-33-0 210713-38-5
210824-35-4 210824-60-5 210824-78-5
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210829-35-9 210829-43-9 210829-57-5
210829-60-0 210829-61-1 238091-55-9
284685-04-7 285555-11-5 285555-30-8
285555-31-9 285555-32-0 285555-43-3
285555-44-4 286369-45-7
RL: PRP (Properties)
(unclaimed sequence; methods using an exendin or related substance for glucagon suppression)

L12 ANSWER 6 OF 9 HCAPLUS COPYRIGHT 2003 ACS
AN 2000:493315 HCAPLUS
DN 133:135612
TI Novel exendin agonist formulations and methods of administration thereof
IN **Young, Andrew**; L'Italien, James J.; Kolterman, Orville
PA **Amylin Pharmaceuticals, Inc., USA**
SO PCT Int. Appl., 281 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 4

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000041546	A2	20000720	WO 2000-US902	20000114 <--
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	CA 2356706	AA	20000720	CA 2000-2356706	20000114 <--
	EP 1140145	A2	20011010	EP 2000-914425	20000114 <--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
	BR 2000007820	A	20011120	BR 2000-7820	20000114 <--
	JP 2002534450	T2	20021015	JP 2000-593167	20000114 <--
	NO 2001003468	A	20010914	NO 2001-3468	20010712 <--
	US 2003087820	A1	20030508	US 2002-157224	20020528 <--
PRAI	US 1999-116380P	P	19990114 <--		
	US 2000-175365P	P	20000110		
	WO 2000-US902	W	20000114		
	US 2001-889330	A2	20011227		

AB Novel exendin and exendin agonist compd. formulations and dosages and methods of administration thereof are provided. These compns. and methods are useful in treating diabetes and conditions that would be benefited by lowering plasma glucose or delaying and/or slowing gastric emptying or inhibiting food intake.
IT **130357-25-4P**, Exendin-3 (Heloderma horridum) **141758-74-9P**
, Exendin-4 (Heloderma suspectum) **210712-28-0P**, 1-30-Exendin 4 (Heloderma suspectum) **210712-29-1P 210712-30-4P**
210712-31-5P 210712-33-7P 210712-36-0P
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210829-43-9P 210829-53-1P 210829-57-5P
210829-60-0P 210829-61-1P 238091-55-9P
239091-09-9P 284676-24-0P 284685-04-7P
RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BSU (Biological study, unclassified); PNU (Preparation, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)
(amino acid sequence; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)

L12 ANSWER 7 OF 9 HCAPLUS COPYRIGHT 2003 ACS
AN 1999:528979 HCAPLUS
DN 131:165747
TI Inotropic and diuretic effects of exendin, glucagon-like peptide-1[7-36]amide, or their agonists
IN **Young, Andrew A.**; Vine, Will; Beeley, Nigel R. A.; Prickett, Kathryn
PA **Amylin Pharmaceuticals, Inc., USA**
SO PCT Int. Appl., 94 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9940788	A1	19990819	WO 1999-US2554	19990205 <--
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2320371	AA	19990819	CA 1999-2320371	19990205 <--
AU 9926596	A1	19990830	AU 1999-26596	19990205 <--
AU 759058	B2	20030403		
EP 1054594	A1	20001129	EP 1999-906762	19990205 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

JP 2002509078 T2 20020326 JP 2000-531064 19990205 <--
PRAI US 1998-75122P P 19980213 <--
WO 1999-US2554 W 19990205
OS MARPAT 131:165747
AB Methods for increasing urine flow are disclosed, comprising administration of an effective amt. of GLP-1, an exendin, or an exendin or GLP-1 agonist. Methods for increasing urinary sodium excretion and decreasing urinary potassium concn. are also disclosed. The methods are useful for treating conditions or disorders assocd. with toxic hypervolemia, such as renal failure, congestive heart failure, nephrotic syndrome, cirrhosis, pulmonary edema, and hypertension. The present invention also relates to methods for inducing an inotropic response comprising administration of an effective amt. of GLP-1, an exendin, or an exendin or GLP-1 agonist. These methods are useful for treating conditions or disorders that can be alleviated by an increase in cardiac contractility such as congestive heart failure. Pharmaceutical compns. for use in the methods of the invention are also disclosed.
IT **165338-05-6P**, 1-31-Exendin 4 (Heloderma suspectum)
210712-28-0P, 1-30-Exendin 4 (Heloderma suspectum)
210712-29-1P 210712-30-4P 210712-31-5P
210712-33-7P 210712-34-8P 210712-36-0P
210712-38-2P 210712-42-8P 210712-50-8P
210712-52-0P 210712-53-1P 210712-54-2P
210712-55-3P 210712-56-4P 210712-57-5P
210712-58-6P 210712-59-7P 210712-60-0P
210712-61-1P 210712-62-2P 210712-64-4P
210712-65-5P 210712-67-7P 210712-68-8P
210824-14-9P 210824-35-4P 210824-60-5P
210824-78-5P 210828-61-8P 210828-91-4P
210828-92-5P 210829-01-9P 210829-03-1P
210829-07-5P 210829-08-6P 210829-11-1P
210829-12-2P 210829-35-9P 210829-36-0P
210829-38-2P 210829-53-1P 210829-57-5P
210829-60-0P 238091-49-1P 238091-54-8P
238091-55-9P 238091-56-0P 238091-57-1P
238091-58-2P 238091-60-6P 238091-62-8P
238091-66-2P 238091-74-2P 238091-76-4P
238091-77-5P 238091-78-6P 238091-79-7P
238091-80-0P 238091-81-1P 238091-82-2P
238091-83-3P 238091-84-4P 238091-85-5P
238091-86-6P 238091-87-7P 238091-89-9P
238091-90-2P 238091-91-3P 238091-92-4P
238091-93-5P 238091-94-6P 238410-89-4P
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238411-08-0P 238411-10-4P 238748-48-6P
239091-09-9P 239091-51-1P 239091-53-3P
239091-57-7P 239091-60-2P 239091-62-4P
239091-64-6P 239100-19-7P
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(inotropic and diuretic effects and synthesis of exendin, glucagon-like peptide-1[7-36]amide, and agonists)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Chen	1996			US 5512549 A	HCAPLUS
Eng	1995			US 5424286 A	HCAPLUS

L12 ANSWER 8 OF 9 HCAPLUS COPYRIGHT 2003 ACS

AN 1998:490528 HCAPLUS
DN 129:149256
TI Preparation of exendin peptides for the reduction of food intake
IN Beeley, Nigel Robert Arnold; Prickett, Kathryn S.; Bhavsar, Sunil
PA **Amylin Pharmaceuticals, Inc., USA**
SO PCT Int. Appl., 214 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	WO 9830231	A1	19980716	WO 1998-US449	19980107	<--
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM					
	RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG					
	AU 9862394	A1	19980803	AU 1998-62394	19980107	<--
	AU 739020	B2	20011004			
	EP 996459	A1	20000503	EP 1998-904545	19980107	<--
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	JP 2002508742	T2	20020319	JP 1998-531147	19980107	<--
	US 2002137666	A1	20020926	US 1998-3869	19980107	<--
	WO 9907404	A1	19990218	WO 1998-US16387	19980806	<--
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	RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG					
	AU 9887729	A1	19990301	AU 1998-87729	19980806	<--
	AU 749914	B2	20020704			
	EP 1019077	A1	20000719	EP 1998-939260	19980806	<--
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	BR 9811866	A	20000815	BR 1998-11866	19980806	<--
	JP 2001513512	T2	20010904	JP 2000-506993	19980806	<--
	CA 2309356	AA	19990527	CA 1998-2309356	19981113	<--
	CA 2310097	AA	19990527	CA 1998-2310097	19981113	<--
	WO 9925727	A2	19990527	WO 1998-US24210	19981113	<--
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	WO 9925728	A1	19990527	WO 1998-US24273	19981113	<--
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM					
	RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI,					

CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

AU 9914046	A1	19990607	AU 1999-14046	19981113	<--
AU 757748	B2	20030306			
AU 9914588	A1	19990607	AU 1999-14588	19981113	<--
AU 756836	B2	20030123			
EP 1032587	A1	20000906	EP 1998-958573	19981113	<--
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BR 9814189	A	20001003	BR 1998-14189	19981113	<--
BR 9815670	A	20001017	BR 1998-15670	19981113	<--
EP 1066314	A1	20010110	EP 1998-957897	19981113	<--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI					
JP 2001523688	T2	20011127	JP 2000-521108	19981113	<--
NZ 504258	A	20021220	NZ 1998-504258	19981113	<--
NZ 504256	A	20030131	NZ 1998-504256	19981113	<--
US 2003087821	A1	20030508	US 2002-187051	20020628	<--
PRAI US 1997-34905P	P	19970107	<--		
US 1997-55404P	P	19970808	<--		
US 1997-65442P	P	19971114	<--		
US 1997-66029P	P	19971114	<--		
US 1998-3869	A1	19980107	<--		
WO 1998-US449	W	19980107	<--		
WO 1998-US16387	W	19980806	<--		
WO 1998-US24210	W	19981113	<--		
WO 1998-US24273	W	19981113	<--		

AB Methods for treating conditions or disorders which can be alleviated by reducing food intake are disclosed which comprise administration of an effective amt. of an exendin or an exendin agonist, alone or in conjunction with other compds. or compns. that effect satiety. Approx. 180 exendin-related peptides were synthesized by the solid-phase method.

IT **210712-52-0P**
RL: FFD (Food or feed use); SPN (Synthetic preparation); BIOL (Biological study); PREP (Preparation); USES (Uses)
(.prepn. of exendin peptides for the redn. of food intake)

IT **158345-16-5P 203743-29-7P 203743-31-1P**
203743-32-2P 203743-33-3P 203743-35-5P
203743-36-6P 203743-37-7P 203743-38-8P
203743-39-9P 203743-40-2P 203743-41-3P
203743-45-7P 203743-46-8P 203743-47-9P
203743-50-4P 203743-53-7P 203743-54-8P
210712-28-0P, 1-30-Exendin 4 (Heloderma suspectum)
210712-29-1P 210712-30-4P 210712-31-5P
210712-32-6P 210712-33-7P 210712-34-8P
210712-36-0P 210712-38-2P 210712-42-8P
210712-50-8P 210712-53-1P 210712-54-2P
210712-55-3P 210712-56-4P 210712-57-5P
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210830-31-2P 210830-35-6P 210830-59-4P
RL: FFD (Food or feed use); SPN (Synthetic preparation); BIOL (Biological study); PREP (Preparation); USES (Uses)
(prepn. of exendin peptides for the redn. of food intake)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Eng	1995			US 5424286 A	HCAPLUS

L12 ANSWER 9 OF 9 HCAPLUS COPYRIGHT 2003 ACS
AN 1998:112250 HCAPLUS
DN 128:192936
TI Preparation of exendin peptide analogs as agonists for regulating gastrointestinal motility
IN **Young, Andrew A.**; **Gedulin, Bronislava**; Beeley, Nigel Robert Arnold; Prickett, Kathryn S.
PA **Amylin Pharmaceuticals, Inc., USA**; Young, Andrew A.; Gedulin, Bronislava; Beeley, Nigel Robert Arnold; Prickett, Kathryn S.
SO PCT Int. Appl., 70 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	WO 9805351	A1	19980212	WO 1997-US14199	19970808	<--
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM					
	RW: GH, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG					
	AU 9740636	A1	19980225	AU 1997-40636	19970808	<--
	EP 966297	A1	19991229	EP 1997-938261	19970808	<--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI					
	JP 2001501593	T2	20010206	JP 1998-508263	19970808	<--
PRAI	US 1996-694954	A	19960808	<--		
	WO 1997-US14199	W	19970808	<--		

OS MARPAT 128:192936
AB Methods for reducing gastric motility and delaying gastric emptying for therapeutic and diagnostic purposes are disclosed which comprise administration of an effective amt. of an exendin or an exendin agonist H-Xaa1-Xaa2-Xaa3-Gly-Thr-Xaa4-Xaa5-Xaa6-Xaa7-Xaa8-Ser-Lys-Gln-Xaa9-Glu-Glu-Glu-Ala-Val-Arg-Leu-Xaa10-Xaa11-Xaa12-Xaa13-Leu-Lys-Asn-Gly-Gly-Xaa14-Ser-Ser-Gly-Ala-Xaa15-Xaa16-Xaa17-Xaa18-Z [Xaa1 = His, Arg, Tyr; Xaa2 = Ser, Gly, Ala, Thr; Xaa3, Xaa7, Xaa12 = independently Asp, Glu; Xaa4, Xaa10 = independently Phe, Tyr, naphthylalanine; Xaa5, Xaa6 = independently Thr,

Ser; Xaa8, Xaa9 = independently Leu, Ile, Val, pentylglycine, Met; Xaa11 = any group Xaa8, tert-butylglycine; Xaa13 = any group Xaa4, Trp; Xaa14-Xaa17 = independently Pro, homoproline, 3-Hyp, 4-Hyp, thioproline, N-alkylglycine, N-alkylpentylglycine, N-alkylalanine; Xaa18 = Ser, Thr, Tyr; Z = OH, NH2; with the proviso that the compd. does not have the formula of exendin-3 or exendin-4] or a pharmaceutically acceptable salt thereof. Methods for treating conditions assocd. with elevated, inappropriate, or undesired post-prandial blood glucose levels are disclosed which comprise administration of an effective amt. of an exendin or an exendin agonist alone or in conjunction with other anti-gastric emptying agents. Thus, exendin-4 acid and [Leu14,Phe25]-exendin-4, prepd. by std. solid-phase methods on a 4-(2,4-dimethoxyphenyl)-Fmoc-aminomethylphenoxyacetamide norleucine-MBHA resin using 9-fluorenylmethoxycarbonyl (Fmoc)-protected amino acids, inhibited gastric emptying in male HSD rats with EC50 = 0.12 and 0.29 .mu.g. Exendin-4 showed EC50 = 0.27 .mu.g under the same conditions.

IT **130357-25-4P**, Exendin-3 (Heloderma horridum) **141758-74-9P**, Exendin-4 (Heloderma suspectum) **158345-16-5P** **203743-26-4P 203743-27-5P 203743-28-6P** **203743-29-7P 203743-30-0P 203743-31-1P** **203743-32-2P 203743-33-3P 203743-35-5P** **203743-36-6P 203743-37-7P 203743-38-8P** **203743-39-9P 203743-40-2P 203743-41-3P** **203743-42-4P 203743-43-5P 203743-44-6P** **203743-45-7P 203743-46-8P 203743-47-9P** **203743-48-0P 203743-49-1P 203743-50-4P** **203743-51-5P 203743-52-6P 203743-53-7P** **203743-54-8P 203743-55-9P**

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(prepn. of exendin peptide analogs as agonists for regulating gastrointestinal motility)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Amylin Pharmaceuticals	1995			WO 9507098	
Bayer	1996	42	1361	Clinical Chemistry	
Chernish	1973			US 3862301 A	HCAPLUS
Daniel	1974	3	720	Br Med J	MEDLINE
Dupre	1995	44	626	Diabetes	HCAPLUS
D'Alessio	1994	93	2263	J Clin Invest	HCAPLUS
Hellstrom	1993	28	38	Scand J Gastroentero	
Miholic	1991		429	Chirurgisches Forum	HCAPLUS
Nauck	1995	38	A39	Diabetologia, Abstra	
Rai	1993	265	G118	Am Physiol J	MEDLINE
Schirra	1995	108	A1003	Gastroenterology	
Schirra	1997	109	84	Proceedings of the A	HCAPLUS

=> d l14 bib abs hitrn retable tot

L14 ANSWER 1 OF 9 HCAPLUS COPYRIGHT 2003 ACS
AN 2003:300601 HCAPLUS
DN 138:298126
TI Compositions and methods for treating peripheral vascular disease with GLP-1 compounds
IN Hathaway, David R.; Coolidge, Thomas R.
PA USA
SO U.S. Pat. Appl. Publ., 12 pp., Cont.-in-part of U.S. Ser. No. 851,738.
CODEN: USXXCO
DT **Patent**

LA English
FAN.CNT 4

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	US 2003073626	A1	20030417	US 2002-91258	20020305	
	US 6284725	B1	20010904	US 1999-302596	19990430	<--
	US 2002055460	A1	20020509	US 2001-851738	20010509	<--
PRAI	US 1999-302596	A3	19990430			
	US 2001-851738	A2	20010509			
	US 1998-103498P	P	19981008	<--		

AB The present invention relates to methods of treating intermittent claudication comprising administering glucagon-like peptide-1 (GLP-1) mols. to subjects suffering therefrom. A method of treating or preventing skeletal muscle injury caused by ischemia and/or reperfusion in a subject comprising the step of administering a therapeutically effective amt. of GLP-1 mol. is also claimed. The subject can also be administered free radical scavengers, glucose, or potassium. The GLP-1 compd. is administered by an infusion pump or by s.c. injection of a slow-release formulation.

IT **510788-20-2**
RL: PRP (Properties)
(unclaimed protein sequence; compns. and methods for treating peripheral vascular disease with GLP-1 compds.)

L14 ANSWER 2 OF 9 HCAPLUS COPYRIGHT 2003 ACS
AN 2001:650487 HCAPLUS
DN 135:205920
TI Metabolic intervention with GLP-1 to improve the function of ischemic and reperfused tissue
IN Coolidge, Thomas R.; Ehlers, Mario R. W.
PA BioNebraska, Inc., USA
SO U.S., 10 pp.
CODEN: USXXAM
DT **Patent**
LA English
FAN.CNT 4

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	US 6284725	B1	20010904	US 1999-302596	19990430	<--
	WO 2000066138	A2	20001109	WO 2000-US11251	20000427	
	WO 2000066138	A3	20010705			
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	EP 1173197	A2	20020123	EP 2000-926404	20000427	
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	NZ 514610	A	20020927	NZ 2000-514610	20000427	
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	US 2002147131	A1	20021010	US 2001-953021	20010911	<--
	NO 2001005294	A	20011228	NO 2001-5294	20011029	
	US 2003073626	A1	20030417	US 2002-91258	20020305	
PRAI	US 1998-103498P	P	19981008	<--		
	US 1999-302596	A	19990430			
	WO 2000-US11251	W	20000427			
	US 2001-851738	A1	20010509			

AB Individuals in need of treatment of ischemia-related reperfusion are treated, preferably i.v., with a compn. which includes a compd. which binds to a receptor for the glucagon-like peptide-1. The invention relates to both the method and compns. for such treatment.

IT **203743-40-2 306277-48-5**
RL: PRP (Properties)
(unclaimed protein sequence; metabolic intervention with GLP-1 to improve the function of ischemic and reperfused tissue)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Anon	1994			WO 94/15925	HCAPLUS
Anon	1998			WO 98/08531	HCAPLUS
Anon	1998			WO 98/08873	HCAPLUS
Apstein	1998	98	2223	Circulation	MEDLINE
Hoover	2000			US 6107329	HCAPLUS
Mishra	1999			US 5955594	HCAPLUS
Tiholiz	1980			US 4196196	HCAPLUS

L14 ANSWER 3 OF 9 HCAPLUS COPYRIGHT 2003 ACS
AN 2000:790326 HCAPLUS
DN 133:345167
TI Metabolic intervention with GLP-1 or its biologically active analogues to improve the function of the ischemic and reperfused brain
IN Coolidge, Thomas R.; Ehlers, Mario R. W.
PA Bionebraska, Inc., USA
SO PCT Int. Appl., 19 pp.
CODEN: PIXXD2
DT **Patent**
LA English
FAN.CNT 4

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000066142	A2	20001109	WO 2000-US11652	20000501
	WO 2000066142	A3	20020124		
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	US 6429197	B1	20020806	US 1999-303016	19990430 <--
	EP 1187628	A2	20020320	EP 2000-928616	20000501
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
	JP 2002543145	T2	20021217	JP 2000-615026	20000501
	NO 2001005298	A	20011228	NO 2001-5298	20011029
PRAI	US 1999-303016	A	19990430		
	US 1998-103498P	P	19981008 <--		
	WO 2000-US11652	W	20000501		

AB It has now been discovered that GLP-1 treatment after acute stroke or hemorrhage, preferably i.v. administration, can be an ideal treatment because it provides a means for optimizing insulin secretion, increasing brain anabolism, enhancing insulin effectiveness by suppressing glucagon, and maintaining euglycemia or mild hypoglycemia with no risk of severe hypoglycemia.

IT **203743-40-2 306277-48-5**
RL: PRP (Properties)
(unclaimed protein sequence; metabolic intervention with GLP-1 or its

biol. active analogs to improve the function of the ischemic and reperfused brain)

L14 ANSWER 4 OF 9 HCAPLUS COPYRIGHT 2003 ACS
AN 2000:790323 HCAPLUS
DN 133:345166
TI Metabolic intervention with GLP-1 to improve the function of ischemic and reperfused tissue
IN Coolidge, Thomas R.; Ehlers, Mario R. W.
PA Bionebraska, Inc., USA
SO PCT Int. Appl., 22 pp.
CODEN: PIXXD2
DT **Patent**
LA English
FAN.CNT 4

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000066138	A2	20001109	WO 2000-US11251	20000427
	WO 2000066138	A3	20010705		
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	US 6284725	B1	20010904	US 1999-302596	19990430 <--
	EP 1173197	A2	20020123	EP 2000-926404	20000427
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
	NZ 514610	A	20020927	NZ 2000-514610	20000427
	JP 2002543142	T2	20021217	JP 2000-615022	20000427
	NO 2001005294	A	20011228	NO 2001-5294	20011029
PRAI	US 1999-302596	A	19990430		
	US 1998-103498P	P	19981008 <--		
	WO 2000-US11251	W	20000427		

AB Individuals in need of treatment of ischemia-related reperfusion are treated, preferably i.v., with a compn. which includes a compd. which binds to a receptor for the glucagon-like peptide-1. The invention relates to both the method and compns. for such treatment.
IT **203743-40-2**
RL: PRP (Properties)
(unclaimed protein sequence; metabolic intervention with GLP-1 to improve the function of ischemic and reperfused tissue)
IT **306277-48-5**
RL: PRP (Properties)
(unclaimed sequence; metabolic intervention with GLP-1 to improve the function of ischemic and reperfused tissue)

L14 ANSWER 5 OF 9 HCAPLUS COPYRIGHT 2003 ACS
AN 2000:133809 HCAPLUS
DN 132:175839
TI Differentiation of non-insulin producing cells into insulin producing cells by GLP-1 or Exendin-4 and uses thereof
IN Egan, Josephine; Perfetti, Riccardo; Passaniti, Antonino; Greig, Nigel; Holloway, Harold
PA United States of America, Department of Health and Human Services, USA
SO PCT Int. Appl., 119 pp.
CODEN: PIXXD2
DT **Patent**
LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000009666	A2	20000224	WO 1999-US18099	19990810 <--
	WO 2000009666	A3	20001123		
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	CA 2339326	AA	20000224	CA 1999-2339326	19990810 <--
	AU 9955524	A1	20000306	AU 1999-55524	19990810 <--
	EP 1105460	A2	20010613	EP 1999-942066	19990810 <--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
PRAI	US 1998-95917P	P	19980810 <--		
	WO 1999-US18099	W	19990810		

AB The present invention relates to a population of insulin producing cells made by a process comprising contacting non-insulin producing cells with a growth factor selected from the group consisting of GLP-1 or Exendin-4, growth factors having amino acid sequences substantially homologous to GLP-1 or Exendin-4, and fragments thereof. The present invention also relates to methods of differentiating non-insulin producing cells into insulin producing cells and of enriching a population of cells for insulin-producing cells. The present invention also relates to methods of treating diabetes. Exendin-4 was more potent an insulinotropic agent than GLP-1 on several levels when given i.v.

IT **203743-40-2 238411-01-3 238411-05-7**
238411-07-9 238411-10-4 238748-48-6
259141-41-8
RL: PRP (Properties)
(unclaimed protein sequence; differentiation of non-insulin producing cells into insulin producing cells by GLP-1 or Exendin-4 and uses thereof)

IT **165338-05-6**, 1-31-Exendin 4 (Heloderma suspectum)
210712-28-0, 1-30-Exendin 4 (Heloderma suspectum)
238091-78-6
RL: PRP (Properties)
(unclaimed sequence; differentiation of non-insulin producing cells into insulin producing cells by GLP-1 or Exendin-4 and uses thereof)

L14 ANSWER 6 OF 9 HCAPLUS COPYRIGHT 2003 ACS
AN 1999:566077 HCAPLUS
DN 131:194808
TI GLP-1 derivatives of GLP-1 and exendin with a protracted profile of action
IN Knudsen, Liselotte Bjerre; Huusfeldt, Per Olaf; Nielsen, Per Franklin; Madsen, Kjeld
PA Novo Nordisk A/s, Den.
SO PCT Int. Appl., 70 pp.
CODEN: PIXXD2
DT **Patent**
LA English

FAN.CNT 11

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9943708	A1	19990902	WO 1999-DK86	19990225 <--
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN,				

MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,
TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU,
TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK,
ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG,
CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

AU 9932477	A1	19990915	AU 1999-32477	19990225	<--
EP 1056775	A1	20001206	EP 1999-936077	19990225	<--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, PT, IE, FI					
ZA 9901571	A	19990902	ZA 1999-1571	19990226	<--
US 2001047084	A1	20011129	US 2001-886311	20010621	<--
PRAI DK 1998-274	A	19980227	<--		
US 1998-84357P	P	19980505	<--		
WO 1999-DK86	W	19990225			
US 1999-312177	B1	19990514			

AB The present invention relates to derivs. exendin and of GLP-1(7-C), wherein C is 35 or 36, which derivs. have just one lipophilic substituent which is attached to the C-terminal amino acid residue. The derivs. have a protracted action relative to GLP-1(7-37) and are useful for treating insulin-dependent and noninsulin-dependent diabetes mellitus. The derivs. of the invention can be combined with other antidiabetics or oral hypoglycemic agents. Pharmaceutical formulations contg. the derivs. of the invention are also claimed.

IT **165338-05-6DP**, 1-31-Exendin 4 (Heloderma suspectum), lipophilic derivs. **165338-06-7DP**, lipophilic derivs.
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(GLP-1 and exendin lipophilic derivs. with a protracted profile for treating diabetes mellitus and obesity)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Boehringer Mannheim Gmb	1997			WO 9746584 A1	HCAPLUS
Buckley, D	1996			US 5545618 A	HCAPLUS
Efendic, S	1997			US 5631224 A	HCAPLUS
Habener, J	1997			US 5614492 A	HCAPLUS
John Eng	1995			US 5424286 A	HCAPLUS
Novo Nordisk AS	1996			WO 9629342 A1	HCAPLUS
Novo Nordisk AS	1998			WO 9808871 A1	HCAPLUS
Protein Delivery Inc	1994			WO 9426778 A1	HCAPLUS
The General Hospital Co	1987			WO 8706941 A1	HCAPLUS
The General Hospital Co	1990			WO 9011296 A1	HCAPLUS

L14 ANSWER 7 OF 9 HCAPLUS COPYRIGHT 2003 ACS
AN 1998:550504 HCAPLUS
DN 129:185369
TI Polynucleotides encoding proexendin, and methods and uses thereof
IN Drucker, Daniel J.
PA 1149336 Ontario Inc., Can.
SO PCT Int. Appl., 27 pp.
CODEN: PIXXD2
DT **Patent**
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI WO 9835033	A1	19980813	WO 1998-CA71	19980204	<--

W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT,

UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG

AU 9858507 A1 19980826 AU 1998-58507 19980204 <--
EP 981611 A1 20000301 EP 1998-901908 19980204 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI
JP 2001512307 T2 20010821 JP 1998-533455 19980204 <--
PRAI US 1997-37412P P 19970205 <--
GB 1997-2582 A 19970207 <--
WO 1998-CA71 W 19980204 <--

AB Exendin 4 is a biol. active peptide first isolated from Gila monster venom. The invention encompasses polynucleotides encoding proexendin peptides, including exendin and novel peptides, as well as isolated or recombinant proexendin peptides. The invention also includes antibodies which specifically recognize such peptides.

IT **211430-73-8**, Exendin ENTP (Heloderma horridum)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence of mature; gene encoding proexendin from Heloderma horridum and applications)

IT **188265-76-1**, Exendin 4, pro- (Heloderma suspectum)
203743-40-2 211430-62-5
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; gene encoding proexendin from Heloderma horridum and applications)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Chen, Y	1997	272	4108	THE JOURNAL OF BIOLO	HCAPLUS
Eng, J	1995			US 5424286 A	HCAPLUS
Eng, J	1992	267	7402	JOURNAL OF BIOLOGICA	HCAPLUS
Pohl, M	1997	112	A1181	GASTROENTEROLOGY, SU	

L14 ANSWER 8 OF 9 HCAPLUS COPYRIGHT 2003 ACS
AN 1998:1503 HCAPLUS
DN 128:48508
TI Exendin analogs, processes for their preparation and medicaments containing them
IN Hoffmann, Eike; Goke, Rudiger; Goke, Burkhard-Johannes
PA Boehringer Mannheim G.m.b.H., Germany; Hoffmann, Eike; Goke, Rudiger; Goke, Burkhard-Johannes
SO PCT Int. Appl., 150 pp.
CODEN: PIXXD2
DT **Patent**
LA German
FAN.CNT 1

PATENT NO. KIND DATE APPLICATION NO. DATE

PI WO 9746584 A1 19971211 WO 1997-EP2930 19970605 <--
W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG
DE 19622502 A1 19980102 DE 1996-19622502 19960605 <--
DE 19637230 A1 19980319 DE 1996-19637230 19960913 <--

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     AU 9731732         A1   19980105       AU 1997-31732    19970605 <--
     AU 723694          B2   20000831
     EP 915910          A1   19990519       EP 1997-927143   19970605 <--
        R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, PT, IE, FI
     BR 9710452         A    19990817       BR 1997-10452    19970605 <--
     CN 1227567         A    19990901       CN 1997-197091   19970605 <--
     JP 2000516912      T2   20001219       JP 1998-500235   19970605 <--
PRAI DE 1996-19622502   A    19960605  <--
     DE 1996-19637230   A    19960913  <--
     WO 1997-EP2930     W    19970605  <--
OS   MARPAT 128:48508
AB   The invention concerns novel exendin analogs which can be used in the
     treatment of diabetes mellitus.  The invention also concerns processes for
     prepg. these substances and medicaments contg. them.  The exendin analogs
     are derived from HSDGTFTSDLSKQMEEEAVRLFIEWLKNGX1 or
     HGEGTFTSDLSKQMEEEAVRLFIEWLKNGX1, where X1 is a (non)proteogenic amino acid
     other than glycine.  These analogs show better decompn. and metabolic
     stability and longer action than GLP-1 or exendin-3, resulting in fewer
     doses being administered.
IT   199729-16-3P 199729-17-4P 199729-18-5P
     199729-19-6P 199729-22-1P 199729-25-4P
     199729-26-5P 199729-27-6P 199729-28-7P
     199729-29-8P 199729-33-4P 199729-35-6P
     199729-40-3P 199729-50-5P
     RL: BAC (Biological activity or effector, except adverse); BSU (Biological
     study, unclassified); SPN (Synthetic preparation); THU (Therapeutic use);
     BIOL (Biological study); PREP (Preparation); USES (Uses)
        (prepn. of exendin analogs and medicaments contg. them for treatment of
        diabetes mellitus)

L14  ANSWER 9 OF 9  HCAPLUS  COPYRIGHT 2003 ACS
AN   1995:675100  HCAPLUS
DN   123:74913
TI   Exendin-3 and exendin-4 polypeptides, and pharmaceutical compositions
     comprising them
IN   Eng, John
PA   USA
SO   U.S., 17 pp.
     CODEN: USXXAM
DT   Patent
LA   English
FAN.CNT 1
     PATENT NO.         KIND  DATE           APPLICATION NO.  DATE
     ---------------    ----  --------       ---------------  --------
PI   US 5424286          A    19950613       US 1993-66480    19930524 <--
PRAI US 1993-66480            19930524  <--
AB   This invention encompasses pharmaceutical compns. contg. exendin-3 or
     exendin-4, fragments thereof, or any combination thereof, and methods for
     the treatment of diabetes mellitus and the prevention of hyperglycemia.
IT   130357-25-4, Exendin 3 (Heloderma horridum) 141758-74-9,
     Exendin 4 (Heloderma suspectum) 165338-05-6, 1-31-Exendin 4
     (Heloderma suspectum) 165338-06-7
     RL: BAC (Biological activity or effector, except adverse); BSU (Biological
     study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL
     (Biological study); USES (Uses)
        (exendin-3 and exendin-4 polypeptides, and pharmaceutical compns.
        comprising them)


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L15  ANSWER 1 OF 10  HCAPLUS  COPYRIGHT 2003 ACS
AN   1999:18104  HCAPLUS
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DN 130:178590
TI Black widow spider .alpha.-latrotoxin: a presynaptic neurotoxin that shares structural homology with the glucagon-like peptide-1 family of insulin secretagogic hormones
AU Holz, George G.; Habener, Joel F.
CS Diabetes Unit, Howard Hughes Medical Institute, Massachusetts General Hospital, Harvard Medical School, Boston, MA, 02114, USA
SO Comparative Biochemistry and Physiology, Part B: Biochemistry & Molecular Biology (**1998**), 121B(2), 177-184
CODEN: CBPBB8; ISSN: 0305-0491
PB Elsevier Science Inc.
DT Journal
LA English
AB .alpha.-Latrotoxin is a presynaptic neurotoxin isolated from the venom of the black widow spider Latrodectus tredecimguttatus. It exerts toxic effects in the vertebrate central nervous system by depolarizing neurons, by increasing [Ca2+]i and by stimulating uncontrolled exocytosis of neurotransmitters from nerve terminals. The actions of .alpha.-latrotoxin are mediated, in part, by a GTP-binding protein-coupled receptor referred to as CIRL or latrophilin. Exendin-4 is also a venom toxin, and it is derived from the salivary gland of the Gila monster Heloderma suspectum. It acts as an agonist at the receptor for glucagon-like peptide-1(7-36)-amide (GLP-I), thereby stimulating secretion of insulin from pancreatic .beta.-cells of the islets of Langerhans. Here is reported a surprising structural homol. between a-latrotoxin and exendin-4 that is also apparent amongst all members of the GLP-1-like family of secretagogic hormones (GLP-1, glucagon, vasoactive intestinal polypeptide, secretin, pituitary adenylyl cyclase activating polypeptide). On the basis of this homol., we report the synthesis and initial characterization of a chimeric peptide (Black Widow GLP-1) that stimulates Ca2+ signaling and insulin secretion in human .beta.-cells and MIN6 insulinoma cells. It is also reported here that the GTP-binding protein-coupled receptors for .alpha.-latrotoxin and exendin-4 share highly significant structural similarity in their extracellularly-oriented amino-termini. We propose that mol. mimicry has generated conserved structural motifs in secretagogic toxins and their receptors, thereby explaining the evolution of defense or predatory strategies that are shared in common amongst distantly related species including spiders, lizards, and snakes. Evidently, the toxic effects of .alpha.-latrotoxin and exendin-4 are explained by their ability to interact with GTP-binding protein-coupled receptors that normally mediate the actions of endogenous hormones or neuropeptides.
IT **141758-74-9**, Exendin 4 (Heloderma suspectum)
RL: PRP (Properties)
(latrotoxin shares structural homol. with glucagon-like peptide-1 family of insulin secretagogic hormones)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Adelhorst, K	1994	269	6275	J Biol Chem	HCAPLUS
Banks, B	1974	45	457	Eur J Biochem	HCAPLUS
Barden, J	1997	272	29572	J Biol Chem	HCAPLUS
Barnett, D	1996	432	1039	Pfluger's Arch	HCAPLUS
Bergwitz, C	1996	271	26469	J Biol Chem	HCAPLUS
Chen, Y	1997	272	4108	J Biol Chem	HCAPLUS
Couvineau, A	1995	206	246	Biochem Biophys Res	HCAPLUS
Davletov, B	1996	271	23239	J Biol Chem	HCAPLUS
Dufton, A	1989	10	258	Trends Pharmacol Sci	
Dulubova, I	1996	271	7535	J Biol Chem	HCAPLUS
Eng, J	1992	267	7402	J Biol Chem	HCAPLUS
Gallwitz, B	1996	63	17	Regul Pept	HCAPLUS
Gaudin, P	1996	805	585	Ann NY Acad Sci	HCAPLUS

Goke, R	1993	268	19650	J Biol Chem	MEDLINE
Graziano, M	1996	4	9	Recept Channel	HCAPLUS
Grishin, E	1996	391	231	Adv Exp Med Biol	HCAPLUS
Hauert, J	1974	6	201	Int J Pept Protein R	HCAPLUS
Hjorth, S	1994	269	30121	J Biol Chem	HCAPLUS
Holz, G	1995	270	17749	J Biol Chem	HCAPLUS
Holz, G	1993	361	362	Nature	HCAPLUS
Holz, G	1992	17	388	Trends Biochem Sci	HCAPLUS
Kiyatkin, N	1993	213	121	Eur J Biochem	HCAPLUS
Kiyatkin, N	1990	270	127	FEBS Lett	
Kolakowski, L	1994	2	1	Recept Channel	HCAPLUS
Krasnoperov, V	1997	18	925	Neuron	HCAPLUS
Lang, L	1998	17	648	EMBO J	
Lelianova, V	1997	272	21504	J Biol Chem	HCAPLUS
Michelena, P	1997	502	481	J Physiol	HCAPLUS
Montrose-Rafizadeh, C	1997	272	21201	J Biol Chem	HCAPLUS
Parker, D	1984	259	11751	J Biol Chem	HCAPLUS
Parker, J				J Biol Chem (in pres	
Petrenko, A	1991	353	65	Nature	HCAPLUS
Rosenthal, L	1989	42	115	Pharmacol Ther	HCAPLUS
Strydom, A	1973	328	491	Biochim Biophys Acta	HCAPLUS
Thorens, B	1993	42	1678	Diabetes	HCAPLUS
Thornton, K	1994	33	3532	Biochemistry	HCAPLUS
Turton, M	1996	379	69	Nature	HCAPLUS
Vandermeers, A	1984	166	273	FEBS Lett	HCAPLUS
Wilmen, A	1997	18	301	Peptides	HCAPLUS
Yang, C	1996	391	85	Adv Exp Med Biol	HCAPLUS

L15 ANSWER 2 OF 10 HCAPLUS COPYRIGHT 2003 ACS
AN 1998:287874 HCAPLUS
DN 129:78077
TI Molecular cloning of the helodermin and exendin-4 cDNAs in the lizard. Relationship to vasoactive intestinal polypeptide/pituitary adenylate cyclase activating polypeptide and glucagon-like peptide 1 and evidence against the existence of mammalian homologues
AU Pohl, Markus; Wank, Stephen A.
CS Digestive Diseases Branch, NIDDK, Natl. Inst. of Health, Bethesda, MD, 20892, USA
SO Journal of Biological Chemistry (**1998**), 273(16), 9778-9784
CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB Helodermin and exendin-4, two peptides isolated from the salivary gland of the Gila monster, Heloderma suspectum, are approx. 50% homologous to vasoactive intestinal peptide (VIP) and glucagon-like peptide-1 (GLP-1), resp., and interact with the mammalian receptors for VIP and GLP-1 with equal or higher affinity and efficacy. Immunohistochem. studies suggested the presence of helodermin-like peptides in mammals. To det. whether helodermin and exendin-4 are present in mammals and their evolutionary relationship to VIP and GLP-1, their cDNAs were first cloned from Gila monster salivary gland. Northern blots and reverse transcription-polymerase chain reaction of multiple Gila monster tissues identified .apprx.500-base pair transcripts only from salivary gland. Both helodermin and exendin-4 full-length cDNAs were .apprx.500 base pairs long, and they encoded precursor proteins contg. the entire amino acid sequence of helodermin and exendin-4, as well as a 44- or 45-amino acid N-terminal extension peptide, resp., having .apprx.60% homol. The size and structural organization of these cDNAs indicated that they are closely related to one another but markedly different from known cDNAs for the VIP/GLP-1 peptide family previously identified in both lower and higher evolved species. Cloning of the Gila monster VIP/peptide histidine isoleucine, pituitary adenylate cyclase activating polypeptide, and

glucagon/GLP-1 cDNAs and Southern blotting of Gila monster DNA demonstrate the coexistence of sep. genes for these peptides and suggests, along with the restricted salivary gland expression, that helodermin and exendin-4 coevolved to serve a sep. specialized function. Probing of a variety of rat and human tissues on Northern blots, human and rat Southern blots, and genomic and cDNA libraries with either helodermin- or exendin-4-specific cDNAs failed to identify evidence for mammalian homologs. These data indicate that helodermin and exendin-4 are not the precursors to VIP and GLP-1 and that they belong to a sep. peptide family encoded by sep. genes. Furthermore, the existence of as yet undiscovered mammalian homologs to helodermin and exendin-4 seems unlikely.

IT **141758-74-9**, Exendin 4 (Heloderma suspectum) **188265-76-1**
, Exendin 4, pro- (Heloderma suspectum)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; mol. cloning and sequence of the helodermin and exendin-4 cDNAs in the Gila monster)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Andrews, P	1980	19	5494	Biochemistry	HCAPLUS
Bertaccini, G	1976	28	127	Pharmacol Rev	HCAPLUS
Bjartell, A	1989	26	27	Regul Pept	HCAPLUS
Chen, Y	1997	272	4108	J Biol Chem	HCAPLUS
Dimaline, R	1988	527	621	Ann N Y Acad Sci	
Drucker, D	1988	263	13475	J Biol Chem	HCAPLUS
Eng, J	1992	267	7402	J Biol Chem	HCAPLUS
Fehmann, H	1994	15	453	Peptides	HCAPLUS
Feurle, G	1992	267	22305	J Biol Chem	HCAPLUS
Goke, R	1993	268	19650	J Biol Chem	MEDLINE
Gourlet, P	1991	1066	245	Biochim Biophys Acta	HCAPLUS
Grunditz, T	1989	86	1357	Proc Natl Acad Sci U	HCAPLUS
Han, J	1987	26	1617	Biochemistry	HCAPLUS
Heinrich, G	1984	115	2176	Endocrinology	HCAPLUS
Hoshino, M	1984	178	233	FEBS Lett	HCAPLUS
Irwin, D	1995	9	267	Mol Endocrinol	HCAPLUS
Iwasaki, S	1995	270	6997	J Biol Chem	HCAPLUS
Karn, R	1993	31	307	Biochem Genet	HCAPLUS
Kimura, C	1990	166	81	Biochem Biophys Res	HCAPLUS
Koham, D	1993	265	F670	Am J Physiol	
Krane, I	1988	263	13317	J Biol Chem	HCAPLUS
Lutz, E	1993	334	3	FEBS Lett	HCAPLUS
McDonald, T	1979	90	227	Biochem Biophys Res	HCAPLUS
McFarlin, D	1995	154	211	Gene	HCAPLUS
McRory, J	1995	108	169	Mol Cell Endocrinol	HCAPLUS
Minamino, N	1983	114	541	Biochem Biophys Res	HCAPLUS
Moro, O	1997	272	966	J Biol Chem	HCAPLUS
Nagalla, S	1992	267	6916	J Biol Chem	HCAPLUS
Nishizawa, M	1985	183	55	FEBS Lett	HCAPLUS
Ogi, K	1990	173	1271	Biochem Biophys Res	HCAPLUS
Parker, D	1984	259	11751	J Biol Chem	HCAPLUS
Raufman, J	1982	242	G470	Am J Physiol	HCAPLUS
Raufman, J	1996	61	1	Reg Pept	HCAPLUS
Robberecht, P	1985	130	333	Biochem Biophys Res	HCAPLUS
Robberecht, P	1985	190	142	FEBS Lett	HCAPLUS
Schepp, W	1994	269	183	Eur J Pharmacol	HCAPLUS
Schweitz, H	1992	267	13928	J Biol Chem	HCAPLUS
Shima, K	1996	63	99	Regul Pept	HCAPLUS
Spindel, E	1990	87	9813	Proc Natl Acad Sci	HCAPLUS
Takasaki, C	1992	189	1527	Biochem Biophys Res	HCAPLUS
Taylor, W	1980	94	9	Biochem Biophys Res	HCAPLUS
Tsutsumi, Y	1990	31	11	Regul Pept	HCAPLUS

Vandermeers, A	1987	164	321	Eur J Biochem	HCAPLUS
Wang, Y	1993	14	573	Peptides	HCAPLUS
Williams, D	1991	175	556	Biochem Biophys Res	HCAPLUS

L15 ANSWER 3 OF 10 HCAPLUS COPYRIGHT 2003 ACS
AN 1997:577997 HCAPLUS
DN 127:257827
TI Novel signal transduction and peptide specificity of glucagon-like peptide receptor in 3T3-L1 adipocytes
AU Montrose-Rafizadeh, Chahrzad; Yang, Huan; Wang, Yihong; Roth, Jesse; Montrose, Marshall H.; Adams, Lisa G.
CS Laboratory of Clinical Physiology, Gerontology Research Center, National Institute on Aging, NIH, Baltimore, MD, USA
SO Journal of Cellular Physiology (**1997**), 172(3), 275-283
CODEN: JCLLAX; ISSN: 0021-9541
PB Wiley-Liss
DT Journal
LA English
AB Glucagon-like peptide-1 (7-36) amide (GLP-1), in addn. to its well known effect of enhancing glucose-mediated insulin release, has been shown to have insulinomimetic effects and to enhance insulin-mediated glucose uptake and lipid synthesis in 3T3-L1 adipocytes. To elucidate the mechanisms of GLP-1 action in these cells, the authors studied the signal transduction and peptide specificity of the GLP-1 response. In 3T3-L1 adipocytes, GLP-1 caused a decrease in intracellular cAMP levels which is the opposite to the response obsd. in pancreatic beta cells in response to the same peptide. In 3T3-L1 adipocytes, free intracellular calcium was not modified by GLP-1. Peptide specificity was examd. to help det. if a different GLP receptor isoform was expressed in 3T3-L1 adipocytes vs. beta cells. Peptides with partial homol. to GLP-1 such as GLP-2, GLP-1 (1-36), and glucagon all lowered cAMP levels in 3T3-L1 adipocytes. In addn., an antagonist of pancreatic GLP-1 receptor, exendin-4 (9-39), acted as an agonist to decrease cAMP levels in 3T3-L1 adipocytes as did exendin-4 (1-39), a known agonist for the pancreatic GLP-1 receptor. Binding studies using 125I-GLP-1 also suggest that pancreatic GLP-1 receptor isoform is not responsible for the effect of GLP-1 and related peptides in 3T3-L1 adipocytes. Based on these results, the authors propose that the major form of the GLP receptor in 3T3-L1 adipocytes is functionally different from the pancreatic GLP-1 receptor.
IT **141758-74-9**, Exendin 4 (Heloderma suspectum)
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(signal transduction and peptide specificity of glucagon-like peptide receptor in 3T3-L1 adipocytes)

L15 ANSWER 4 OF 10 HCAPLUS COPYRIGHT 2003 ACS
AN 1997:567059 HCAPLUS
DN 127:257697
TI High potency antagonists of the pancreatic glucagon-like peptide-1 receptor
AU Montrose-Rafizadeh, Chahrzad; Yang, Huan; Rodgers, Buel D.; Beday, Alvie; Pritchette, Louella A.; Eng, John
CS Laboratory of Clinical Physiology, NIA, National Institutes of Health, Baltimore, MD, 21224, USA
SO Journal of Biological Chemistry (**1997**), 272(34), 21201-21206
CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB GLP-1-(7-36)-amide and exendin-4-(1-39) are glucagon-like peptide-1 (GLP-1) receptor agonists, whereas exendin-(9-39) is the only known antagonist. To analyze the transition from agonist to antagonist and to

identify the amino acid residues involved in ligand activation of the GLP-1 receptor, we used exendin analogs with successive N-terminal truncations. Chinese hamster ovary cells stably transfected with the rat GLP-1 receptor were assayed for changes in intracellular cAMP caused by the test peptides in the absence or presence of half-maximal stimulatory doses of GLP-1. N-terminal truncation of a single amino acid reduced the agonist activity of the exendin peptide, whereas N-terminal truncation of 3-7 amino acids produced antagonists that were 4-10-fold more potent than exendin-(9-39). N-terminal truncation of GLP-1 by 2 amino acids resulted in weak agonist activity, but an 8-amino acid N-terminal truncation inactivated the peptide. Binding studies performed using 125I-labeled GLP-1 confirmed that all bioactive peptides specifically displaced tracer with high potency. In a set of exendin/GLP-1 chimeric peptides, substitution of GLP-1 sequences into exendin-(3-39) produced loss of antagonist activity with conversion to a weak agonist. The results show that receptor binding and activation occur in sep. domains of exendin, but they are more closely coupled in GLP-1.

IT **141758-74-9**, Exendin 4 (Heloderma suspectum)
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(glucagon-like peptide-1 receptor high potency antagonists and structure-activity relations thereof)

L15 ANSWER 5 OF 10 HCAPLUS COPYRIGHT 2003 ACS
AN 1997:127672 HCAPLUS
DN 126:223096
TI Tissue-specific expression of unique mRNAs that encode proglucagon-derived peptides or exendin 4 in the lizard
AU Chen, Yuqing E.; Drucker, Daniel J.
CS Toronto Hosp., Univ. Toronto, Toronto, ON, M5G 2C4, Can.
SO Journal of Biological Chemistry (**1997**), 272(7), 4108-4115
CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB Glucagon-like peptide 1 stimulates insulin secretion and inhibits glucagon secretion, gastric emptying, and feeding, suggesting it may be biol. useful for the treatment of diabetes. A lizard glucagon-like peptide 1(GLP-1)-related peptide, exendin 4, binds to the GLP-1 receptor and mimics the actions of GLP-1 in vivo. To det. the genetic relationship between exendin 4 and GLP-1, the authors analyzed the structure and expression of pancreatic and intestinal proglucagon mRNAs in the reptile Heloderma suspectum. Two different proglucagon cDNAs (lizard proglucagon I (LPI) and lizard proglucagon II (LPII)), with unique 3'-untranslated regions were identified. Two LPI mRNA transcripts, .apprx.1.6 and 2.1 kilobases, encoded glucagon and GLP-1 but not GLP-2 and were restricted in expression to the pancreas. In contrast, a 1.1-kilobase LPII mRNA transcript, encoding glucagon, GLP-1, and GLP-2 utilized a different 3'-untranslated region and was expressed in both pancreas and intestine. Lizard proglucagon mRNA transcripts were not detectable by reverse transcription-polymerase chain reaction or Northern blotting in salivary gland. A single class of lizard salivary gland proexendin cDNAs encoded the sequence of exendin 4 and a 45-amino acid exendin N-terminal peptide. Exendin mRNA transcripts were expressed in the salivary gland, but not pancreas or intestine. These data demonstrate that GLP-1 and exendin 4 represent related yet distinct peptide encoded by different genes in the lizard.

IT **188265-76-1**, Exendin 4, pro- (Heloderma suspectum)
RL: PRP (Properties)
(amino acid sequence; unique mRNAs that encode proglucagon-derived peptides or exendin 4 tissue-specific expression in lizard)

L15 ANSWER 6 OF 10 HCAPLUS COPYRIGHT 2003 ACS
AN 1994:622490 HCAPLUS
DN 121:222490
TI Use of 125I-[Y39]exendin-4 to characterize exendin receptors on dispersed pancreatic acini and gastric chief cells from guinea pig
AU Singh, Gurcharn; Eng, John; Raufman, Jean-Pierre
CS Gastrointestinal Cell Biology Laboratory, State University of New York-Health Science Center at Brooklyn, 450 Clarkson Avenue-Box 1196, Brooklyn, NY, 11203-2098, USA
SO Regulatory Peptides (**1994**), 53(1), 47-59
CODEN: REPPDY; ISSN: 0167-0115
DT Journal
LA English
AB We synthesized and iodinated an exendin-4 analog, [Y39]exendin-4 (700 Ci/mmol), for use as a radioligand to characterize exendin receptors on dispersed pancreatic acini and gastric chief cells from guinea pig. Binding of this bioactive radioligand was rapid, temp.-dependent and specific (not inhibited by other pancreatic or gastric secretagogues). Measurement of the ability of exendin-4 to inhibit the binding of 125I-[Y39]exendin-4 indicated the presence of two classes of receptors. Pancreatic acini had 12.5 .times. 1010 binding sites/mg acinar protein of which 6% were high affinity (Kd = 0.5 nM) and 94% were low affinity (Kd = 0.1 .mu.M). Chief cells had 3370 binding sites/cell of which 9% were high affinity (Kd = 0.3 nM) and 91% were low affinity (Kd = 0.2 .mu.M). Washing with 0.2 M acetic acid (pH 2.5), 0.2 M glycine (pH 10.5), or trypsin (100 .mu.g/mL) after 30 min incubation at 37.degree., indicated that 63 and 49% of radioligand was internalized in acini and chief cells, resp. Truncated glucagon-like peptide-1 (tGLP-1), a mammalian peptide sharing 53% homol. with exendin-4, inhibited radioligand binding at the same concns. that altered secretion from acini and chief cells. Glucagon, GLP-1 and GLP-2 inhibited 125I-[Y39]exendin-4 binding only at concns. .gtoreq.100 nM. Exendin(9-39)NH2, a specific exendin-receptor antagonist, potently inhibited 125I-[Y39] exendin-4 binding (IC50 = 6.1 and 3.5 nM in acini and chief cells, resp.). In pancreatic acini and gastric chief cells from guinea pig, exendin-3, exendin-4 and tGLP-1 increase cellular cAMP and modulate enzyme secretion by interacting with high-affinity exendin receptors. 125I-[Y39] exendin-4 is a useful radioligand for studying exendin receptors.
IT **130357-25-4**, Exendin 3 (Heloderma horridum) **141758-74-9**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(cAMP formation and enzyme secretion by pancreas acinus and stomach chief cells response to)
IT **158345-16-5P**
RL: RCT (Reactant); SPN (Synthetic preparation); PREP (Preparation); RACT (Reactant or reagent)
(prepn. and radioiodination of)
IT **158345-15-4P 158345-17-6P**
RL: SPN (Synthetic preparation); PREP (Preparation)
(prepn. as radioligand for extendin receptors)

L15 ANSWER 7 OF 10 HCAPLUS COPYRIGHT 2003 ACS
AN 1993:597526 HCAPLUS
DN 119:197526
TI Exendin-4 is a high potency agonist and truncated exendin-(9-39)-amide an antagonist at the glucagon-like peptide 1-(7-36)-amide receptor of insulin-secreting .beta.-cells
AU Goeke, Ruediger; Fehmann, Hans Christoph; Linn, Thomas; Schmidt, Harald; Krause, Michael; Eng, John; Goeke, Burkhard
CS Dep. Intern. Med., Philipps Univ., Marburg, 3550, Germany
SO Journal of Biological Chemistry (**1993**), 268(26), 19650-5
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal

LA English
AB Exendin-4 purified from Heloderma suspectum venom shows structural relationship to the important incretin hormone glucagon-like peptide 1-(7-36)-amide (GLP-1). The authors demonstrate that exendin-4 and truncated exendin-(9-39)-amide specifically interact with the GLP-1 receptor on insulinoma-derived cells and on lung membranes. Exendin-4 displaced 125I-GLP-1, and unlabeled GLP-1 displaced 125I-exendin-4 from the binding site at rat insulinoma-derived RINm5F cells. Exendin-4 had, like GLP-1, a pronounced effect on intracellular cAMP generation, which was reduced by exendin-(9-39)-amide. When combined, GLP-1 and exendin-4 showed additive action on cAMP. They each competed with the radiolabeled version of the other peptide in crosslinking expts. The apparent mol. mass of the resp. ligand-binding protein complex was 63,000 Da. Exendin-(9-39)-amide abolished the crosslinking of both peptides. Exendin-4, like GLP-1, stimulated dose dependently the glucose-induced insulin secretion in isolated rat islets, and, in mouse insulinoma .beta.TC-1 cells, both peptides stimulated the proinsulin gene expression at the level of transcription. Exendin-(9-39)-amide reduced these effects. In conclusion, exendin-4 is an agonist and exendin-(9-39)-amide is a specific GLP-1 receptor antagonist.
IT **141758-74-9**
RL: BIOL (Biological study)
(glucagon-like peptide 1-(7-36)-amide receptor of .beta.-cells and lung response to)

L15 ANSWER 8 OF 10 HCAPLUS COPYRIGHT 2003 ACS
AN 1992:564310 HCAPLUS
DN 117:164310
TI Truncated glucagon-like peptide-1 interacts with exendin receptors on dispersed acini from guinea pig pancreas. Identification of a mammalian analogue of the reptilian peptide exendin-4
AU Raufman, Jean Pierre; Singh, Latika; Singh, Gurcharn; Eng, John
CS Health Sci. Cent., State Univ. New York, Brooklyn, NY, 11203-2098, USA
SO Journal of Biological Chemistry (**1992**), 267(30), 21432-7
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB To find mammalian analogs of exendin-4, a peptide from Helodermatidae venoms that interacts with newly discovered exendin receptors on dispersed acini from guinea pig pancreas, the actions of glucagon-like peptide-1 [GLP-1(1-37)], its truncated form GLP-1(7-36)NH2, GLP-2(1-34), and pituitary adenylate cyclase-activating peptide were examd. and compared with secretin, VIP, and glucagon. Only the truncated form of glucagon-like peptide-1, GLP-1(7-36)NH2 mimicked the actions of exendin-4. Like exendin-4, GLP-1(7-36)NH2 increased acinar cAMP without stimulating amylase release. GLP-1(7-36)NH2-induced increases in cAMP were inhibited progressively by increasing concns. of the specific exendin-receptor antagonist, exendin(9-39)NH2. In dispersed acini from guinea pig and rat pancreas, concns. of GLP-1(7-36)NH2 that stimulated increases in cAMP caused potentiation of cholecystokinin-induced amylase release. Binding of 125I-[Y39]exendin-4 or 125I-GLP-1(7-36)NH2 to dispersed acini from guinea pig pancreas was inhibited by adding increasing concns. of unlabeled exendin-4 or GLP-1(7-36)NH2. Thus, the mammalian peptide GLP-1(7-36)NH2 interacts with exendin receptors on dispersed acini from guinea pig pancreas. Exendin(9-39)NH2, a competitive antagonist of the actions of GLP-1(7-36)NH2 in pancreatic acini, may be a useful tool for examg. the physiol. actions of this peptide.
IT **141758-74-9**
RL: BIOL (Biological study)
(glucagon-like peptide 1 truncated form as mammalian analog of)

L15 ANSWER 9 OF 10 HCAPLUS COPYRIGHT 2003 ACS
AN 1992:402472 HCAPLUS

DN 117:2472
TI Isolation and characterization of exendin-4, an exendin-3 analog, from Heloderma suspectum venom. Further evidence for an exendin receptor on dispersed acini from guinea pig pancreas
AU Eng, John; Kleinman, Wayne A.; Singh, Latika; Singh, Gurcharn; Raufman, Jean Pierre
CS Solomon A Berson Res. Lab., Veterans Aff. Med. Cent., Bronx, NY, 10468, USA
SO Journal of Biological Chemistry (**1992**), 267(11), 7402-5
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB An amino acid sequencing assay for peptides contg. an amino-terminal histidine residue (His1) was used to isolate a 39-amino acid peptide, exendin-4, from H. suspectum venom. Exendin-4 differs from exendin-3 by two amino acid substitutions, Gly2-Glu3 in place of Ser2-Asp3, but is otherwise identical. The structural differences make exendin-4 distinct from exendin-3 in its bioactivity. In dispersed acini from guinea pig pancreas, natural and synthetic exendin-4 stimulate a monophasic increase in cAMP beginning at 100 pM that plateaus at 10 nM. The exendin-4-induced increase in cAMP is inhibited progressively by increasing concns. of the exendin receptor antagonist, exendin-(9-39) amide. Unlike exendin-3, exendin-4 does not stimulate a second rise in acinar cAMP at concns. >100 nM, does not stimulate amylase release, and does not inhibit the binding of radiolabeled vasoactive intestinal peptide to acini. This indicates that in dispersed pancreatic acini, exendin-4 interacts only with the recently described exendin receptor.
IT **141758-74-9**
RL: PRP (Properties)
(amino acid sequence of, complete)

L15 ANSWER 10 OF 10 HCAPLUS COPYRIGHT 2003 ACS
AN 1990:608593 HCAPLUS
DN 113:208593
TI Purification and structure of exendin-3, a new pancreatic secretagogue isolated from Heloderma horridum venom
AU Eng, John; Andrews, P. C.; Kleinman, Wayne A.; Singh, Latika; Raufman, Jean Pierre
CS Solomon A. Berson Res. Lab., Veterans Aff. Med. Cent., Bronx, NY, 10468, USA
SO Journal of Biological Chemistry (**1990**), 265(33), 20259-62
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB An assay for His1 peptides performed by amino-terminal amino acid sequencing was used to screen venom from the Gila monster lizard, H. horridum. Two His1 peptides were identified: helospectin and a new His1 peptide that has been named exendin-3 to indicate that it is the third peptide to be found in an exocrine secretion of Heloderma lizards which has endocrine activity, the first two being helospectin (exendin-1) and helodermin (exendin-2). In the lot of H. horridum venom tested, exendin-3 was 5-10-fold more abundant in molar concn. than helospectin. The structure of exendin-3 was analyzed by amino acid sequencing and mass spectrometry. Exendin-3 is a 39-amino acid peptide with a mass of 4200. It contains a carboxyl-terminal amide and has a strong homol. with secretin at its amino-terminal 12 amino acids. The complete structure of exendin-3 is: His-Ser-Asp-Gly-Thr-Phe-Thr-Ser-Asp-Leu-Ser-Lys-Gln-Met-Glu-Glu-Glu-Ala-Val-Arg-Leu-Phe-Ile-Glu-Trp-Leu-Lys-Asn-Gly-Gly-Pro-Ser-Ser-Gly-Ala-Pro-Pro-Pro-Ser. It is 32 and 26% homologous with helospectin and helodermin, resp. It has greatest homol. with glucagon (48%) and human glucagon-like peptide-1 (50%). Exendin-3 (3 .mu.M) stimulated increases in cellular cAMP and amylase release from dispersed guinea pig pancreatic acini.

IT **130357-25-4**, Exendin 3 (Heloderma horridum)
RL: PRP (Properties)
(amino acid sequence of)

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FILE 'HOME' ENTERED AT 12:32:33 ON 25 JUN 2003

=> index bioscience medicine
FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED
COST IN U.S. DOLLARS                                    SINCE FILE      TOTAL
                                                           ENTRY    SESSION
FULL ESTIMATED COST                                         0.21       0.21

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS,
       BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CANCERLIT,
       CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE,
       DRUGB, DRUGLAUNCH, DRUGMONOG2, ...' ENTERED AT 12:32:51 ON 25 JUN 2003

70 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view
search error messages that display as 0* with SET DETAIL OFF.

=> s exendin (s) glucagon? or (glucagon (w) level#) and (glucagonoma or necrolytic (w0
migratory (w) erytherma) and ( polymer? or PEG?)
MISSING OPERATOR 'ECROLYTIC (W0'
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> s exendin (s) glucagon? or (glucagon (w) level#) and (glucagonoma or necrolytic (w)
migratory (w) erytherma) and ( polymer? or PEG?)
         28   FILE ADISCTI
          7   FILE ADISINSIGHT
          3   FILE ADISNEWS
          5   FILE AGRICOLA
          2   FILE AQUASCI
          2   FILE BIOCOMMERCE
        184   FILE BIOSIS
          6   FILE BIOTECHABS
          6   FILE BIOTECHDS
         50   FILE BIOTECHNO
  12 FILES SEARCHED...
         15   FILE CABA
         23   FILE CANCERLIT
        117   FILE CAPLUS
         22   FILE CIN
  21 FILES SEARCHED...
         60   FILE DDFU
       1025   FILE DGENE
          3   FILE DRUGNL
         64   FILE DRUGU
          2   FILE DRUGUPDATES
  30 FILES SEARCHED...
          7   FILE EMBAL
        137   FILE EMBASE
        119   FILE ESBIOBASE
          2*  FILE FEDRIP
          2   FILE FROSTI
          5   FILE IFIPAT
          5   FILE JICST-EPLUS
         24   FILE LIFESCI
  44 FILES SEARCHED...
         67   FILE MEDLINE
          1   FILE OCEAN
         70   FILE PASCAL
          1   FILE PHAR
          4   FILE PHARMAML
          8   FILE PHIN
         20   FILE PROMT
  58 FILES SEARCHED...
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        169   FILE SCISEARCH
         29   FILE TOXCENTER
         72   FILE USPATFULL
          6   FILE USPAT2
         24   FILE WPIDS
  66 FILES SEARCHED...
         24   FILE WPINDEX
          3   FILE IPA
         14   FILE NLDB

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L1   QUE EXENDIN (S) GLUCAGON? OR (GLUCAGON (W) LEVEL#) AND (GLUCAGONOMA OR NEC
       ROLYTIC (W) MIGRATORY (W) ERYTHERMA) AND (POLYMER? OR PEG?)

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=> s l1
L2 1025 FILE DGENE
L3 184 FILE BIOSIS
L4 169 FILE SCISEARCH
L5 137 FILE EMBASE
L6 119 FILE ESBIOBASE
L7 117 FILE CAPLUS
L8 72 FILE USPATFULL
L9 70 FILE PASCAL
L10 67 FILE MEDLINE
L11 64 FILE DRUGU
L12 50 FILE BIOTECHNO
L13 29 FILE TOXCENTER
L14 28 FILE ADISCTI
L15 24 FILE LIFESCI
L16 24 FILE WPIDS
L17 23 FILE CANCERLIT
L18 22 FILE CIN
L19 20 FILE PROMT
L20 15 FILE CABA
L21 14 FILE NLDB
L22 8 FILE PHIN
L23 7 FILE ADISINSIGHT
L24 7 FILE EMBAL
L25 6 FILE BIOTECHDS
L26 6 FILE USPAT2
L27 5 FILE AGRICOLA
L28 5 FILE IFIPAT
L29 5 FILE JICST-EPLUS
L30 4 FILE PHARMAML
L31 3 FILE ADISNEWS
L32 3 FILE DRUGNL
L33 3 FILE IPA
L34 2 FILE AQUASCI
L35 2 FILE BIOCOMMERCE
L36 2 FILE DRUGUPDATES
L37 2 FILE FROSTI
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'EXENDIN (S) GLUCAGON?'
L38 2 FILE FEDRIP
L39 1 FILE OCEAN
L40 1 FILE PHAR

TOTAL FOR ALL FILES
L41 2347 L1

```
=> s exendin (s) glucagon? or (glucagon (w) level#) (s) (glucagonoma or necrolytic (w)
migratory (w) erytherma) and (( polymer? (s) exendin?)  or PEG? (s) exendin?))
UNMATCHED RIGHT PARENTHESIS 'EXENDIN?))'
The number of right parentheses in a query must be equal to the
number of left parentheses.

=> s exendin (s) glucagon? or (glucagon (w) level#) (s) (glucagonoma or necrolytic (w)
migratory (w) erytherma) and (( polymer? (s) exendin?)  or ( PEG? (s) exendin?))
L42        1025 FILE DGENE
L43         184 FILE BIOSIS
L44         169 FILE SCISEARCH
L45         137 FILE EMBASE
L46         119 FILE ESBIOBASE
L47         117 FILE CAPLUS
L48          69 FILE USPATFULL
L49          70 FILE PASCAL
L50          67 FILE MEDLINE
L51          64 FILE DRUGU
L52          50 FILE BIOTECHNO
L53          29 FILE TOXCENTER
L54          28 FILE ADISCTI
L55          24 FILE LIFESCI
L56          24 FILE WPIDS
L57          23 FILE CANCERLIT
L58          22 FILE CIN
L59          20 FILE PROMT
L60          15 FILE CABA
L61          14 FILE NLDB
L62           8 FILE PHIN
L63           7 FILE ADISINSIGHT
L64           7 FILE EMBAL
L65           6 FILE BIOTECHDS
L66           6 FILE USPAT2
L67           5 FILE AGRICOLA
L68           5 FILE IFIPAT
L69           5 FILE JICST-EPLUS
L70           4 FILE PHARMAML
L71           3 FILE ADISNEWS
L72           3 FILE DRUGNL
L73           3 FILE IPA
L74           2 FILE AQUASCI
L75           2 FILE BIOCOMMERCE
L76           2 FILE DRUGUPDATES
L77           2 FILE FROSTI
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'EXENDIN (S) GLUCAGON?'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'LEVEL#) (S) '
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'POLYMER? (S) EXENDIN?'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'PEG? (S) EXENDIN?'
L78           2 FILE FEDRIP
L79           1 FILE OCEAN
L80           1 FILE PHAR

TOTAL FOR ALL FILES
L81        2344 EXENDIN (S) GLUCAGON? OR (GLUCAGON (W) LEVEL#) (S) (GLUCAGONOMA
                OR NECROLYTIC (W) MIGRATORY (W) ERYTHERMA) AND ((POLYMER? (S)
                EXENDIN?) OR (PEG? (S) EXENDIN?))

=> s exendin-4 (s) glucagon? or (glucagon (w) level#) (s) (glucagonoma or necrolytic (w)
migratory (w) erytherma)(( polymer? (s) exendin-4)  or ( PEG? (s) exendin-4))
MISSING OPERATOR
MISSING OPERATOR ERYTHERMA)((
```

The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> sexendin-4 (s) glucagon? or (glucagon (w) level#) (s) (glucagonoma or necrolytic (w)
migratory (w) erytherma) and ((polymer? (s) exendin-4) or (PEG? (s) exendin-4))
SEXENDIN-4 IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s exendin-4 (s) glucagon? or (glucagon (w) level#) (s) (glucagonoma or necrolytic (w)
migratory (w) erytherma) and ((polymer? (s) exendin-4) or (PEG? (s) exendin-4))
L82 456 FILE DGENE
L83 109 FILE BIOSIS
L84 110 FILE SCISEARCH
L85 85 FILE EMBASE
L86 72 FILE ESBIOBASE
L87 78 FILE CAPLUS
L88 42 FILE USPATFULL
L89 44 FILE PASCAL
L90 42 FILE MEDLINE
L91 51 FILE DRUGU
L92 32 FILE BIOTECHNO
L93 17 FILE TOXCENTER
L94 25 FILE ADISCTI
L95 12 FILE LIFESCI
L96 16 FILE WPIDS
L97 14 FILE CANCERLIT
L98 20 FILE CIN
L99 13 FILE PROMT
L100 4 FILE CABA
L101 10 FILE NLDB
L102 7 FILE PHIN
L103 5 FILE ADISINSIGHT
L104 5 FILE EMBAL
L105 4 FILE BIOTECHDS
L106 5 FILE USPAT2
L107 2 FILE AGRICOLA
L108 4 FILE IFIPAT
L109 2 FILE JICST-EPLUS
L110 4 FILE PHARMAML
L111 2 FILE ADISNEWS
L112 2 FILE DRUGNL
L113 3 FILE IPA
L114 1 FILE AQUASCI
L115 1 FILE BIOCOMMERCE
L116 2 FILE DRUGUPDATES
L117 1 FILE FROSTI
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'EXENDIN-4 (S) GLUCAGON?'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'LEVEL#) (S) '
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'POLYMER? (S) EXENDIN-4'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'PEG? (S) EXENDIN-4'
L118 2 FILE FEDRIP
L119 0 FILE OCEAN
L120 1 FILE PHAR

TOTAL FOR ALL FILES
L121 1305 EXENDIN-4 (S) GLUCAGON? OR (GLUCAGON (W) LEVEL#) (S) (GLUCAGONOM
A OR NECROLYTIC (W) MIGRATORY (W) ERYTHERMA) AND ((POLYMER? (S)
EXENDIN-4) OR (PEG? (S) EXENDIN-4))

```
=> s  exendin (s) glucagon? or (glucagon (w) level#) (s)(( polymer? (s) exendin-4)  or (
PEG? (s) exendin-4))
L122      1025 FILE DGENE
L123       184 FILE BIOSIS
L124       169 FILE SCISEARCH
L125       137 FILE EMBASE
L126       119 FILE ESBIOBASE
L127       117 FILE CAPLUS
L128        69 FILE USPATFULL
<------User Break------>

SEARCH ENDED BY USER
SEARCH ENDED BY USER

=> s exendin-4 (s) (glucagon? or (glucagon (w) level#)) (s) (( polymer? (s) exendin-4)
or ( PEG? (s) exendin-4))
L129         0 FILE DGENE
L130         2 FILE BIOSIS
L131         2 FILE SCISEARCH
L132         2 FILE EMBASE
L133         2 FILE ESBIOBASE
L134         0 FILE CAPLUS
L135         1 FILE USPATFULL
L136         0 FILE PASCAL
L137         0 FILE MEDLINE
L138         1 FILE DRUGU
L139         2 FILE BIOTECHNO
L140         0 FILE TOXCENTER
L141         0 FILE ADISCTI
L142         2 FILE LIFESCI
L143         1 FILE WPIDS
L144         0 FILE CANCERLIT
L145         0 FILE CIN
L146         0 FILE PROMT
L147         0 FILE CABA
L148         0 FILE NLDB
L149         0 FILE PHIN
L150         1 FILE ADISINSIGHT
L151         0 FILE EMBAL
L152         2 FILE BIOTECHDS
L153         0 FILE USPAT2
L154         0 FILE AGRICOLA
L155         0 FILE IFIPAT
L156         0 FILE JICST-EPLUS
L157         0 FILE PHARMAML
L158         0 FILE ADISNEWS
L159         0 FILE DRUGNL
L160         0 FILE IPA
L161         0 FILE AQUASCI
L162         0 FILE BIOCOMMERCE
L163         0 FILE DRUGUPDATES
L164         0 FILE FROSTI
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'EXENDIN-4 (S) '
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'POLYMER? (S) EXENDIN-4'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'PEG? (S) EXENDIN-4'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED ') (S) '
L165         0 FILE FEDRIP
L166         0 FILE OCEAN
L167         0 FILE PHAR

TOTAL FOR ALL FILES
```

```
L168         18 EXENDIN-4 (S) (GLUCAGON? OR (GLUCAGON (W) LEVEL#)) (S) ((POLYMER
                ? (S) EXENDIN-4) OR (PEG? (S) EXENDIN-4))

=> s exendin-4 (s) (glucagon? or (glucagon (w) level#)) and  (( polymer? (s) exendin-4)
or ( PEG? (s) exendin-4)) and (glucagonoma or necrolytic (w) migratory (w) erytherma)
L169          0 FILE DGENE
L170          0 FILE BIOSIS
L171          0 FILE SCISEARCH
L172          0 FILE EMBASE
L173          0 FILE ESBIOBASE
L174          0 FILE CAPLUS
L175          0 FILE USPATFULL
L176          0 FILE PASCAL
L177          0 FILE MEDLINE
L178          0 FILE DRUGU
L179          0 FILE BIOTECHNO
L180          0 FILE TOXCENTER
L181          0 FILE ADISCTI
L182          0 FILE LIFESCI
L183          1 FILE WPIDS
L184          0 FILE CANCERLIT
L185          0 FILE CIN
L186          0 FILE PROMT
L187          0 FILE CABA
L188          0 FILE NLDB
L189          0 FILE PHIN
L190          0 FILE ADISINSIGHT
L191          0 FILE EMBAL
L192          0 FILE BIOTECHDS
L193          0 FILE USPAT2
L194          0 FILE AGRICOLA
L195          0 FILE IFIPAT
L196          0 FILE JICST-EPLUS
L197          0 FILE PHARMAML
L198          0 FILE ADISNEWS
L199          0 FILE DRUGNL
L200          0 FILE IPA
L201          0 FILE AQUASCI
L202          0 FILE BIOCOMMERCE
L203          0 FILE DRUGUPDATES
L204          0 FILE FROSTI
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'EXENDIN-4 (S) '
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'POLYMER? (S) EXENDIN-4'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'PEG? (S) EXENDIN-4'
L205          0 FILE FEDRIP
L206          0 FILE OCEAN
L207          0 FILE PHAR

TOTAL FOR ALL FILES
L208          1 EXENDIN-4 (S) (GLUCAGON? OR (GLUCAGON (W) LEVEL#)) AND ((POLYMER
                ? (S) EXENDIN-4) OR (PEG? (S) EXENDIN-4)) AND (GLUCAGONOMA OR
                NECROLYTIC (W) MIGRATORY (W) ERYTHERMA)

=> d l208 ibib abs

L208 ANSWER 1 OF 1  WPIDS (C) 2003 THOMSON DERWENT
ACCESSION NUMBER:      2000-490999 [43]    WPIDS
CROSS REFERENCE:       2000-514584 [46]; 2001-514422 [56]
DOC. NO. CPI:          C2000-147547
TITLE:                 Lowering plasma glucagon using exendin, an exendin
                       agonist, a modified exendin or a modified exendin
                       agonist, useful for treating hyperglucagonemia and
```

diabetes.
DERWENT CLASS: A25 A96 B04
INVENTOR(S): GEDULIN, B; YOUNG, A
PATENT ASSIGNEE(S): (AMYL-N) AMYLIN PHARM INC
COUNTRY COUNT: 91
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000041548	A2	20000720	(200043)*	EN	96
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ TZ UG ZW					
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
AU 2000024136	A	20000801	(200054)		
NO 2001003469	A	20010914	(200163)		
EP 1143989	A2	20011017	(200169)	EN	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI					
BR 2000007823	A	20011120	(200202)		
KR 2001086165	A	20010908	(200219)		
KR 2002001719	A	20020109	(200246)		
CN 1347327	A	20020501	(200252)		
JP 2002538084	W	20021112	(200275)		104

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000041548	A2	WO 2000-US942	20000114
AU 2000024136	A	AU 2000-24136	20000114
NO 2001003469	A	WO 2000-US942	20000114
		NO 2001-3469	20010712
EP 1143989	A2	EP 2000-902415	20000114
		WO 2000-US942	20000114
BR 2000007823	A	BR 2000-7823	20000114
		WO 2000-US942	20000114
KR 2001086165	A	KR 2001-708904	20010713
KR 2002001719	A	WO 2000-US942	20000114
		KR 2001-708892	20010713
CN 1347327	A	CN 2000-805017	20000114
JP 2002538084	W	JP 2000-593169	20000114
		WO 2000-US942	20000114

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2000024136	A	Based on	WO 200041548
EP 1143989	A2	Based on	WO 200041548
BR 2000007823	A	Based on	WO 200041548
KR 2002001719	A	Based on	WO 200041548
JP 2002538084	W	Based on	WO 200041548

PRIORITY APPLN. INFO: US 2000-175365P 20000110; US 1999-116380P 19990114; US 1999-132017P 19990430
AN 2000-490999 [43] WPIDS
CR 2000-514584 [46]; 2001-514422 [56]
AB WO 200041548 A UPAB: 20021120
NOVELTY - A new method for lowering plasma glucagon comprises administering a compound (C1) selected from exendin, an exendin agonist, a modified exendin or a modified exendin agonist.
ACTIVITY - Antidiabetic; dermatological.

MECHANISM OF ACTION - The compounds lower plasma glucagon level.

The safety, tolerability, and efficacy of synthetic **exendin -4** was evaluated in 8 male non-insulin using patients with type 2 diabetes who had discontinued other antidiabetic therapy for a minimum of 7 days. Each patient received subcutaneous (SC) injections of placebo (PBO) and 0.1, 0.2, and 0.3 micro g/kg **exendin-4** 48 hours apart in a single-blind, dose-rising, placebo controlled crossover design. Five patients also received a 0.4 micro g/kg dose. Plasma glucose, insulin and **glucagon** concentrations were assessed during fasting and in response to a 7 Kcal/kg Sustacal (RTM) challenge administered at the time of **exendin-4**/PBO injection. Gastric emptying was evaluated by measuring serum acetaminophen concentrations following a 20 mg/kg oral dose of liquid acetaminophen administered with the Sustacal (RTM).

No safety issues were identified based upon reported adverse events, EKG (undefined) and safety lab monitoring. Doses of 0.3 and 0.4 micro g/kg elicited a dose-dependent increase in nausea. Vomiting occurred at the highest dose.

Plasma glucose concentrations were reduced in all doses of **exendin-4** compared to PBO although insulin concentrations were not significantly different. The 8 hour mean plus or minus SE changes in plasma glucose AUC (undefined) from baseline were +391 plus or minus 187, -263 plus or minus 108, -247 plus or minus 64, -336 plus or minus 139, and -328 plus or minus 70 (mg)(hr)/dL for the PBO, 0.1, 0.2, 0.3, and 0.4 micro g/kg doses respectively. The 3 hour changes in plasma **glucagon** were +128.0 plus or minus 19.2, -5.6 plus or minus 10.5, -29.4 plus or minus 18.6, -40.5 plus or minus 24.5, and +6.9 plus or minus 38.6 (pg)(hr)/mL respectively. The gastric emptying rate was slowed in all doses and the mean total absorbed acetaminophen over 6 hours was reduced by 51%, 50%, 57% and 79% compared to PBO for 0.1, 0.2, 0.3, and 0.4 micro g/kg doses respectively.

In summary, SC injection of **exendin-4** to patients identified no safety issues, was tolerated at doses at most 0.3 micro g/kg, reduced plasma glucose and **glucagon** and slowed the rate of gastric emptying.

USE - The method is useful for lowering plasma glucagon in subjects, preferably humans, suffering from necrolytic erythema or **glucagonoma** (claimed). The method is also useful for treating hyperglucagonemia and other conditions that would benefit from reduced glucagon levels and/or suppression of glucagon, e.g. type 1 and type 2 diabetes.

Dwg.0/6

```
=> s exendin-4 (s) (glucagon? or (glucagon (w) level#)) and  (( polymer? (s) exendin-4)
or ( PEG? (s) exendin-4))
L209          0 FILE DGENE
L210          2 FILE BIOSIS
L211          2 FILE SCISEARCH
L212          2 FILE EMBASE
L213          2 FILE ESBIOBASE
L214          0 FILE CAPLUS
L215          1 FILE USPATFULL
L216          0 FILE PASCAL
L217          0 FILE MEDLINE
L218          1 FILE DRUGU
L219          2 FILE BIOTECHNO
L220          0 FILE TOXCENTER
L221          0 FILE ADISCTI
L222          2 FILE LIFESCI
L223          2 FILE WPIDS
L224          0 FILE CANCERLIT
L225          0 FILE CIN
L226          0 FILE PROMT
L227          0 FILE CABA
```

```
L228          0 FILE NLDB
L229          0 FILE PHIN
L230          1 FILE ADISINSIGHT
L231          0 FILE EMBAL
L232          2 FILE BIOTECHDS
L233          0 FILE USPAT2
L234          0 FILE AGRICOLA
L235          0 FILE IFIPAT
L236          0 FILE JICST-EPLUS
L237          0 FILE PHARMAML
L238          0 FILE ADISNEWS
L239          0 FILE DRUGNL
L240          0 FILE IPA
L241          0 FILE AQUASCI
L242          0 FILE BIOCOMMERCE
L243          0 FILE DRUGUPDATES
L244          0 FILE FROSTI
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'EXENDIN-4 (S) '
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'POLYMER? (S) EXENDIN-4'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'PEG? (S) EXENDIN-4'
L245          0 FILE FEDRIP
L246          0 FILE OCEAN
L247          0 FILE PHAR

TOTAL FOR ALL FILES
L248         19 EXENDIN-4 (S) (GLUCAGON? OR (GLUCAGON (W) LEVEL#)) AND ((POLYMER
                ? (S) EXENDIN-4) OR (PEG? (S) EXENDIN-4))

=> rem dup l248
DUP IS NOT VALID HERE
The DELETE command is used to remove various items stored by the
system.

To delete a saved query, saved answer set, saved L-number list, SDI
request, batch request, mailing list, or user-defined cluster, format,
or search field, enter the name.  The name may include ?  for left,
right, or simultaneous left and right truncation.

Examples:

  DELETE BIO?/Q           - delete query names starting with BIO
  DELETE ?DRUG/A          - delete answer set names ending with DRUG
  DELETE ?ELEC?/L         - delete L-number lists containing ELEC
  DELETE ANTICOAG/S       - delete SDI request
  DELETE ENZYME/B         - delete batch request
  DELETE .MYCLUSTER       - delete user-defined cluster
  DELETE .MYFORMAT        - delete user-defined display format
  DELETE .MYFIELD         - delete user-defined search field
  DELETE NAMELIST MYLIST - delete mailing list

To delete an ordered document or an offline print, enter its
number.

Examples:

  DELETE P123001C         - delete print request
  DELETE D134002C         - delete document order request

To delete an individual L-number or range of L-numbers, enter the
L-number or L-number range.  You may also enter DELETE LAST followed
by a number, n, to delete the last n L-numbers.  RENUMBER or
NORENUMBER may also be explicitly specified to override the value of
```

SET RENUMBER.

Examples:

```
  DELETE L21             - delete a single L-number
  DELETE L3-L6           - delete a range of L-numbers
  DELETE LAST 4          - delete the last 4 L-numbers
  DELETE L33-            - delete L33 and any higher L-number
  DELETE -L55            - delete L55 and any lower L-number
  DELETE L2-L6 RENUMBER - delete a range of L-numbers and
                          renumber remaining L-numbers
  DELETE RENUMBER        - renumber L-numbers after deletion of
                          intermediate L-numbers
```

Entire sets of saved items, SDI requests, batch requests, user-defined items, or E-numbers can be deleted.

Examples:

```
  DELETE SAVED/Q - delete all saved queries
  DELETE SAVED/A - delete all saved answer sets
  DELETE SAVED/L - delete all saved L-number lists
  DELETE SAVED   - delete all saved queries, answer sets,
                   and L-number lists
  DELETE SAVED/S - delete all SDI requests
  DELETE SAVED/B - delete all batch requests
  DELETE CLUSTER - delete all user-defined clusters
  DELETE FORMAT  - delete all user-defined display formats
  DELETE FIELD   - delete all user-defined search fields
  DELETE SELECT  - delete all E-numbers
  DELETE HISTORY - delete all L-numbers and restart the
                   session at L1
```

To delete an entire multifile SDI request, enter DELETE and the name of the request. To delete a component from the multifile SDI, enter DELETE and the name of the component.

```
=> dup rem l248
DUPLICATE IS NOT AVAILABLE IN 'DGENE, ADISINSIGHT, PHARMAML, ADISNEWS,
BIOCOMMERCE, DRUGUPDATES, FEDRIP, PHAR'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L248
L249           9 DUP REM L248 (10 DUPLICATES REMOVED)

=> d l249 1-9 ibib abs
NO VALID FORMATS ENTERED FOR FILE 'ADISINSIGHT'
In a multifile environment, each file must have at least one valid
format requested.  Refer to file specific help messages or the
STNGUIDE file for information on formats available in individual
files.
REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):so au ti abs

L249  ANSWER 1 OF 9  BIOTECHDS COPYRIGHT 2003 THOMSON DERWENT AND ISI
AU    GREIG N H; EGAN J; DOYLE M; HOLLOWAY H; PERRY T A
TI    New Glucagon-like peptide-1 or exendin-2 polypeptides, or their
      analogues, useful for treating a subject with diabetes or a
      neurodegenerative condition (e.g. Alzheimer's disease, stroke, multiple
      sclerosis or brain injury);
         recombinant glucagon-like protein preparation for disease therapy
AN    2003-12947  BIOTECHDS
AB    DERWENT ABSTRACT:
      NOVELTY - A purified polypeptide, which comprises the amino acid sequence
      of Glucagon-like peptide-1 (GLP-1), GLP-1 analogue, exendin-2
      or an exendin analogue with a spacer between the amino acid residues
      comparable to residues 7 and 8, or residues 8 and 9 of GLP-1, is new. The
```

polypeptide comprises of any of 22 sequences having 28, 30, 33, 35, 37 or 39 amino acids fully defined in the specification.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following: (1) reducing neuronal death, promoting neuronal differentiation or proliferation, or promoting growth of neuronal processes, by contacting one or more neurons with the polypeptide; and (2) reducing formation or accumulation of amyloid protein by contacting one or more neurons with the polypeptide, which affects amyloid precursor protein metabolism.

BIOTECHNOLOGY - Preferred Polypeptide: The polypeptide is insulinotropic. The spacer is a 6-aminohexanoic acid spacer, which comprises less than four 6-aminohexanois acid residues. The polypeptide may further comprise any of 10 sequences having 30, 31, 39, 40, 43 or 46 amino acids fully defined in the specification. Preferred Method: The contacting cited in the methods of (2) is conducted in vivo or in vitro . Preparation: The peptides can be prepared using standard recombinant techniques.

ACTIVITY - Antidiabetic; Nootropic; Neuroprotective; Antiparkinsonian; Anticonvulsant; Cerebroprotective. Whole brain homogenates were assayed for amyloid-beta (Abeta) 1-40 levels following intracerebroventricular infusions of GLP-1, **exendin-4** , NGF or vehicle in normal control mice. After 48 hours, all animals were sacrificed, the brains removed and rapidly frozen in liquid nitrogen. Brains were pulverized and stored (-80degreesC) prior to assaying for Abeta levels. Equivalent volumes of conditioned media and whole brain homogenate were assayed for Abeta1-40 using a sandwich ELISA. The monoclonal antibody BAN50 (raised against Abeta1-16) was used as the capture antibody for species of Abeta (Abeta1-20 and Abeta1-42). All treatments reduced the levels of Abeta1-40 compared to vehicle. Multiple comparisons following significant main effects of treatment demonstrated that Abeta1-40 levels were reduced significantly following 6.6 mug GLP1 (36%, p less than 0.01) treatment.

MECHANISM OF ACTION - Insulinotropic; Insulin Agonist.

USE - The polypeptides are useful for treating a subject with diabetes (particularly type 2 diabetes) or a neurodegenerative condition (e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, stroke, multiple sclerosis, brain injury, spinal cord injury or peripheral neuropathy), as well as for reducing the symptom(s) of neurodegenerative conditions in a subject. The polypeptide is also useful for reducing neuronal death (which is caused by a neurodegenerative condition, a toxin or an injury), promoting neuronal differentiation or proliferation, promoting growth of neuronal processes, reducing formation or accumulation of amyloid protein. The polypeptides are also useful for treating a subject with neurotoxic injury or neurodegenerative condition, or for reducing the symptom(s) of neurotoxic injury or neurodegenerative condition in a subject.

ADMINISTRATION - For in vivo use, the dosage is 0.1 pmoles/kg/minute to 100 nmoles/kg/minute for continuous administration; and 0.01-400 nmoles/kg for bolus injection. Administration is oral, intravenous, intramuscular, intraperitoneal, topical, transdermal, local, systemic, intraventricular, intracerebral, subdural or intrathecal.

EXAMPLE - The peptides were synthesized on a **PEG** -Polystyrene resin using Fmoc derivatives of amino acids. (119 pages)

L249 ANSWER 2 OF 9 USPATFULL

IN Piccariello, Thomas, Blacksburg, VA, UNITED STATES
Olon, Lawrence P., Bristol, TN, UNITED STATES
Kirk, Randal J., Radford, VA, UNITED STATES

TI Active agent delivery systems and methods for protecting and administering active agents

AB A composition comprising a polypeptide and an active agent covalently attached to the polypeptide. Also provided is a method for delivery of an active agent to a patient comprising administering to the patient a composition comprising a polypeptide and an active agent covalently attached to the polypeptide. Also provided is a method for protecting an

active agent from degradation comprising covalently attaching the active agent to a polypeptide. Also provided is a method for controlling release of an active agent from a composition comprising covalently attaching the active agent to the polypeptide.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L249 ANSWER 3 OF 9 BIOTECHDS COPYRIGHT 2003 THOMSON DERWENT AND ISI
AU SHERIDAN S D
TI Inducing stem cell differentiation by treating isolated stem cells with a retinoid such that portion of stem cells differentiate into hepaticopancreatic tissue such as pancreatic tissue, pancreatic endocrine tissue;
diabetic servere combined immmunodeficiency mouse animal model for disease therapy and tissue engineering
AN 2003-09339 BIOTECHDS
AB DERWENT ABSTRACT:
NOVELTY - Inducing (M1) stem cell differentiation by treating isolated stem cells with a retinoid under conditions effective to cause at least a portion of the stem cells to differentiate into hepaticopancreatic tissue, is new.

DETAILED DESCRIPTION - An INDEPENDENT CLAIM is also included for a composition (I) comprising the hepaticopancreatic tissue produced by (M1).

BIOTECHNOLOGY - Preferred Method: The stem cells are obtained from a stem cell source chosen from placenta, bone marrow, adipose tissue, neural tissue, umbilical cord, blastocyst inner cell mass, and germ cells. The retinoid is vitamin A, retinol, retinal, or retinoic acid, preferably retinoic acid. The conditions are effective to differentiate at least 1, preferably 5 % of the stem cells into hepaticopancreatic tissue. The method further involves treating the isolated stem cells with a morphogen such as a member of the **glucagon**-like peptide family, a cAMP raising agent, nicotinamide, a transcription factor, a protein growth factor, or their mixtures. Preferably, the morphogen is chosen from **glucagon**-like peptide (GLP)-1, **exendin-4**, PDX-1, Ngn-3, gastrin, gastrin-releasing peptide, hepatocyte growth factor, betacellulin, or their mixtures. Preferred Composition: (I) comprises hepaticopancreatic tissue which comprises glucose-responsive insulin-producing cells. (I) comprises 1 % or more of the hepaticopancreatic tissue produced by (M1). Preferably (I) comprises 10 % or more of the hepaticopancreatic tissue, and is obtained by purifying the hepaticopancreatic tissue produced by (M1).

ACTIVITY - Antidiabetic; Antiinflammatory; Hepatotropic; Cytostatic. Insulin-producing cells produced by differentiation of embryonic stem (ES) cells were cultured and were stained with the vital dye dithizone (DTZ). DTZ is a specific dye for zinc-containing granules that were especially abundant in differentiated beta-cells and were representative of insulin-containing storage structures. 200-300 DTZ positively stained cell clusters were transplanted under the kidney capsule of streptozotocin (STZ) induced diabetic serve combined immmunodeficient (SCID) mice to evaluate their ability to reverse the diabetic state of the animal. The results showed the ability of retinoic acid-treated differentiated embryonic stem cells to correct the blood glucose levels in STZ-SCID mice after transplantation.

MECHANISM OF ACTION - Cell therapy.

USE - (M1) is useful for inducing differentiation of stem cells (preferably mammalian embryonic stem cells) to hepaticopancreatic tissue such as pancreatic tissue; pancreatic endocrine tissue which comprises insulin-producing cells that are glucose-responsive; or liver tissue. (I) is useful for treating a mammal which involves identifying a mammal having an extraintestinal gastrointestinal disorder (a hepaticopancreatic disorder such as diabetes, pancreatitis, hepatic cirrhosis, hepatitis, cancer, and pancreatico-biliary disease) and administering (I) to the mammal. Preferably, (I) comprises glucose-responsive insulin-producing cells and is useful for treating diabetes in humans. (All claimed.)

ADMINISTRATION - (I) is preferably injected directly into the organ. No dosage is given.

EXAMPLE - Embryonic stem (ES) cell lines were cultured and spilt 1:8 every three days for 4 passages on gelatin coated tissue culture (TC) dishes without mouse embryonic fibroblasts (MEF's) (with 1500 units/ml lymphocyte inhibitory factor (LIF) in media) to remove MEF's from culture. The resulting stem cells were then differentiated as follows. On day 1, the stem cells were treated with trypsin to break up some aggregation and then suspended in 1 % fetal calf serum (FCS) media (without LIF). The stem cell were then allowed to self-aggregated into embryoid bodies in suspension culture. On day 3, the cells were given a fresh media change and then split among two bacterial petri dishes. A solution containing 1 micro-M retinoic acid was intermixed with the sample and both the control (no retinoic acid) and the sample were allowed to incubate at 37 degrees C. Fresh media were supplied at day 5 (with fresh 1 micro-M retinoic acid for the treated sample). At day 7 fresh media was supplied for both, with no retinoic acid (retinoic acid only present from days 3-7). Fresh media was supplied again on day 9. On day 11, the cells were again trypsinized and then placed into TC dishes with 10 % FCS media (no LIF). Small aliquots were taken at various times (days 14, 17, 19, 22 and 25) from the cultures and used for analysis by reverse transcriptase **polymerase** chain reaction (RT-PCR). On day 14, the media was changed for the two groups of cells, in each population (control and sample). On day 17, the media was changed again. On day 19, adherent cells were gently blown off, then trypsinized and resuspended in 10 % FCS in bacterial petri dish suspension cultures. On days 22 and 25, the remaining cells were collected, and a portion retained for RT-PCR analysis. All culturing from day 1 forward was performed in 25 millimolar (mM) glucose (high glucose) until after day 19, when it was changed to 5.5 mM glucose (lower glucose). Total RNA from each aliquot collected above was purified. The presence of specific RNA transcripts (i.e. insulin) was determined by RT-PCR. Total RNA was prepared from cultures of differentiating ES cells. RT-PCR analyses were performed. The RT-PCR results showed that no insulin was produced in any of the control samples, indicating an absence of insulin or amylase producing cells. In contrast, insulin-producing cells resulted when stem cells were treated with retinoic acid, as indicated by the presence of a correctly sized band during gel electrophoresis of insulin-specific RT-PCR generated products of RNA purified from aliquots obtained at days 14, 17, 19 and 22.(19 pages)

L249 ANSWER 4 OF 9 WPIDS (C) 2003 THOMSON DERWENT
IN PRICKETT, K; YOUNG, A
TI Modified exendin or an exendin agonist linked to one or more polyethylene glycol (PEG) polymers, modulate plasma glucose levels, useful for treating disorders such as diabetes and obesity.
AN 2000-672834 [65] WPIDS
AB WO 200066629 A UPAB: 20001214
NOVELTY - A modified exendin (I) or exendin agonist (II) comprising (I) or (II) linked to one or more polyethylene glycol (PEG) polymers, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a method for making (I) or (II) comprising linking one or more PEG polymers to (I) and/or (II);

(2) a method for treating a disease benefited by administration of (I) or (II);

(3) a method of beneficially regulating gastrointestinal motility comprising administering (I) and/or (II);

(4) a method for treatment of ingestion of a toxin comprising administering (I) or (II) to prevent or reduce the passage of stomach contents to the intestines and aspirating the contents of the stomach;

(5) a method for reducing appetite or weight, lowering plasma lipids, treating diabetes mellitus, modulating triglyceride levels, or suppressing glucagon secretion comprising administering (I) and/or (II); and

(6) a pharmaceutical composition for use in the treatment of

conditions or disorders associated with hypernutrition, or in reducing the appetite or weight of a subject, or in suppressing glucagon secretion, or in modulating triglyceride levels comprising administering (I) and/or (II).

ACTIVITY - Anorectic; antidiabetic; hyperglycemic; hypoglycemic.
No relevant biological data is given.
MECHANISM OF ACTION - Exendins modulate plasma glucose levels.
No relevant biological data is given.
USE - (I) and/or (II) are useful for treatment of diabetes and conditions that would be benefited by lowering plasma glucose or delaying and/or slowing gastric emptying or inhibiting food intake such as obesity and eating disorders.
Dwg.0/6

L249 ANSWER 5 OF 9 WPIDS (C) 2003 THOMSON DERWENT
IN GEDULIN, B; YOUNG, A
TI Lowering plasma glucagon using exendin, an exendin agonist, a modified exendin or a modified exendin agonist, useful for treating hyperglucagonemia and diabetes.
AN 2000-490999 [43] WPIDS
CR 2000-514584 [46]; 2001-514422 [56]
AB WO 200041548 A UPAB: 20021120
NOVELTY - A new method for lowering plasma glucagon comprises administering a compound (C1) selected from exendin, an exendin agonist, a modified exendin or a modified exendin agonist.

ACTIVITY - Antidiabetic; dermatological.
MECHANISM OF ACTION - The compounds lower plasma glucagon level.
The safety, tolerability, and efficacy of synthetic **exendin -4** was evaluated in 8 male non-insulin using patients with type 2 diabetes who had discontinued other antidiabetic therapy for a minimum of 7 days. Each patient received subcutaneous (SC) injections of placebo (PBO) and 0.1, 0.2, and 0.3 micro g/kg **exendin-4** 48 hours apart in a single-blind, dose-rising, placebo controlled crossover design. Five patients also received a 0.4 micro g/kg dose. Plasma glucose, insulin and **glucagon** concentrations were assessed during fasting and in response to a 7 Kcal/kg Sustacal (RTM) challenge administered at the time of **exendin-4**/PBO injection. Gastric emptying was evaluated by measuring serum acetaminophen concentrations following a 20 mg/kg oral dose of liquid acetaminophen administered with the Sustacal (RTM).

No safety issues were identified based upon reported adverse events, EKG (undefined) and safety lab monitoring. Doses of 0.3 and 0.4 micro g/kg elicited a dose-dependent increase in nausea. Vomiting occurred at the highest dose.

Plasma glucose concentrations were reduced in all doses of **exendin-4** compared to PBO although insulin concentrations were not significantly different. The 8 hour mean plus or minus SE changes in plasma glucose AUC (undefined) from baseline were +391 plus or minus 187, -263 plus or minus 108, -247 plus or minus 64, -336 plus or minus 139, and -328 plus or minus 70 (mg)(hr)/dL for the PBO, 0.1, 0.2, 0.3, and 0.4 micro g/kg doses respectively. The 3 hour changes in plasma **glucagon** were +128.0 plus or minus 19.2, -5.6 plus or minus 10.5, -29.4 plus or minus 18.6, -40.5 plus or minus 24.5, and +6.9 plus or minus 38.6 (pg)(hr)/mL respectively. The gastric emptying rate was slowed in all doses and the mean total absorbed acetaminophen over 6 hours was reduced by 51%, 50%, 57% and 79% compared to PBO for 0.1, 0.2, 0.3, and 0.4 micro g/kg doses respectively.

In summary, SC injection of **exendin-4** to patients identified no safety issues, was tolerated at doses at most 0.3 micro g/kg, reduced plasma glucose and **glucagon** and slowed the rate of gastric emptying.

USE - The method is useful for lowering plasma glucagon in subjects, preferably humans, suffering from necrolytic erythema or glucagonoma (claimed). The method is also useful for treating hyperglucagonemia and other conditions that would benefit from reduced glucagon levels and/or

suppression of glucagon, e.g. type 1 and type 2 diabetes.
Dwg.0/6

L249 ANSWER 6 OF 9 DRUGU COPYRIGHT 2003 THOMSON DERWENT
SO Exp.Clin.Endocrinol.Diabetes (107, Suppl. 3, S108-S113, 1999) 2 Fig. 38 Ref.
CODEN: ECEDF ISSN: 0947-7349
AV Diabetes-Schulungszentrum, Medizinische Klinik I, Klinikum der Johann Wolfgang Goethe-Universitaet, Theodor-Stern-Kai 7, D- 60590 Frankfurt am Main, Germany. (e-mail: DSZ-Haak@em.uni- frankfurt.de).
AU Haak
TI New developments in the treatment of type 1 diabetes mellitus.
AN 1999-43452 DRUGU T E
AB New developments in the treatment of type 1 diabetes mellitus are reviewed. Insulin delivery, Pseudomassaria induced reversal of clinical signs of diabetes mellitus in mice, studies with insulin analogs (protracted- and fast-acting), glucagon-like peptides and blood glucose monitoring systems are discussed. (conference paper: International Symposium on Autoimmunity and Endocrinology, Frankfurt, Germany, 1999).
ABEX Intrapulmonary insulin delivery has become feasible as a result of the development of high-efficacy nebulizers which provide a sufficient degree of intrapulmonary drug retention. This method of insulin administration has proved safe and efficient in clinical studies. P.o. insulin delivery seems feasible when surface active substances such as bile salts are used as resorption enhancers to cross the mucosal membrane in the gut. Use of zona occludens toxin (produced by Vibrio cholerae) has been reported. Protease inhibitors and **polymer** coatings have been used to protect the insulin molecule against digestive proteolytic activity. Pseudomassaria (L-783281) reverses the clinical signs of diabetes mellitus in mice by binding to the inner part of the insulin receptor and inducing typical insulin effects. Various insulin analogs have been designed and tested for clinical use including long-acting analogs such as HOE 901 and NN 304 and fast-acting lispro and insulin aspart (aimed at improving postprandial glucose regulation). **Glucagon**-like peptide-1 (GLP-1) improves metabolic control by a variety of effects but has a very short half-life. Derivatives with better resistance to degradation have been developed (**exendin-4**). Other approaches include the development of substances which augment endogenous release of GLP-1 and use of valine pyrrolidide to improve glucose tolerance. Various approaches aimed at improving or easing blood glucose self-monitoring have been developed. (E27/SK)

L249 ANSWER 7 OF 9 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 1
SO Journal of Biological Chemistry, (April 17, 1998) Vol. 273, No. 16, pp. 9778-9784.
ISSN: 0021-9258.
AU Pohl, Markus; Wank, Stephen A. (1)
TI Molecular cloning of the helodermin and **exendin-4** cDNAs in the lizard: Relationship to vasoactive intestinal polypeptide/pituitary adenylate cyclase activating polypeptide and **glucagon**-like peptide 1 and evidence against the existence of mammalian homologues.
AB Helodermin and **exendin-4**, two peptides isolated from the salivary gland of the Gila monster, Heloderma suspectum, are approximately 50% homologous to vasoactive intestinal peptide (VIP) and **glucagon**-like peptide-1 (GLP-1), respectively, and interact with the mammalian receptors for VIP and GLP-1 with equal or higher affinity and efficacy. Immunohistochemical studies suggested the presence of helodermin-like peptides in mammals. To determine whether helodermin and **exendin-4** are present in mammals and their evolutionary relationship to VIP and GLP-1, their cDNAs were first cloned from Gila monster salivary gland. Northern blots and reverse transcription-**polymerase** chain reaction of multiple Gila monster tissues identified apprx500-base pair transcripts only from salivary gland. Both helodermin and **exendin-4** full-length cDNAs were

apprx500 base pairs long, and they encoded precursor proteins containing the entire amino acid sequence of helodermin and **exendin-4**, as well as a 44- or 45-amino acid N-terminal extension peptide, respectively, having apprx60% homology. The size and structural organization of these cDNAs indicated that they were closely related to one another but markedly different from known cDNAs for the VIP/GLP-1 peptide family previously identified in both lower and higher evolved species. Cloning of the Gila monster VIP/peptide histidine isoleucine, pituitary adenylate cyclase activating polypeptide, and **glucagon** / GLP-1 cDNAs and Southern blotting of Gila monster DNA demonstrate the coexistence of separate genes for these peptides and suggests, along with the restricted salivary gland expression, that helodermin and **exendin-4** coevolved to serve a separate specialized function. Probing of a variety of rat and human tissues on Northern blots, human and rat Southern blots, and genomic and cDNA libraries with either helodermin- or **exendin-4**-specific cDNAs failed to identify evidence for mammalian homologues. These data indicate that helodermin and **exendin-4** are not the precursors to VIP and GLP-1 and that they belong to a separate peptide family encoded by separate genes. Furthermore, the existence of as yet undiscovered mammalian homologues to helodermin and **exendin-4** seems unlikely.

L249 ANSWER 8 OF 9 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 2
SO Journal of Biological Chemistry, (1997) Vol. 272, No. 7, pp. 4108-4115. ISSN: 0021-9258.
AU Chen, Yuqing E.; Drucker, Daniel J. (1)
TI Tissue-specific expression of unique mRNAs that encode proglucagon-derived peptides or exendin 4 in the lizard.
AB **Glucagon**-like peptide 1 stimulates insulin secretion and inhibits **glucagon** secretion, gastric emptying, and feeding, suggesting it may be biologically useful for the treatment of diabetes. A lizard **glucagon**-like peptide 1 (GLP-1)-related peptide, **exendin 4**, binds to the GLP-1 receptor and mimics the actions of GLP-1 in vivo. To determine the genetic relationship between **exendin 4** and GLP-1, we analyzed the structure and expression of pancreatic and intestinal proglucagon mRNAs in the reptile Heloderma suspectum. Two different proglucagon cDNAs (lizard proglucagon I (LPI) and lizard proglucagon 11 (LPII)), with unique 3'-untranslated regions were identified. Two LPI mRNA transcripts, apprx 1.6 and 2.1 kilobases, encoded **glucagon** and GLP-1 but not GLP-2 and were restricted in expression to the pancreas. In contrast, a 1.1-kilobase LPII mRNA transcript, encoding **glucagon**, GLP-1, and GLP-2 utilized a different 3'-untranslated region and was expressed in both pancreas and intestine. Lizard proglucagon mRNA transcripts were not detectable by reverse transcription-**polymerase** chain reaction or Northern blotting in salivary gland. A single class of lizard salivary gland proexendin cDNAs encoded the sequence of **exendin 4** and a 45-amino acid exendin NH-2-terminal peptide. Exendin mRNA transcripts were expressed in the salivary gland, but not pancreas or intestine. These data demonstrate that GLP-1 and **exendin 4** represent related yet distinct peptides encoded by different genes in the lizard.

L249 ANSWER 9 OF 9 ADISINSIGHT COPYRIGHT (C) 2003 Adis Data Information BV
SO Adis R&D Insight

=>

=> d l249 1-9 ibib abs
NO VALID FORMATS ENTERED FOR FILE 'ADISINSIGHT'
In a multifile environment, each file must have at least one valid format requested. Refer to file specific help messages or the STNGUIDE file for information on formats available in individual files.
REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):so au ti abs

L249 ANSWER 1 OF 9 BIOTECHDS COPYRIGHT 2003 THOMSON DERWENT AND ISI
AU GREIG N H; EGAN J; DOYLE M; HOLLOWAY H; PERRY T A
TI New Glucagon-like peptide-1 or exendin-2 polypeptides, or their analogues, useful for treating a subject with diabetes or a neurodegenerative condition (e.g. Alzheimer's disease, stroke, multiple sclerosis or brain injury);
recombinant glucagon-like protein preparation for disease therapy
AN 2003-12947 BIOTECHDS
AB DERWENT ABSTRACT:
NOVELTY - A purified polypeptide, which comprises the amino acid sequence of **Glucagon**-like peptide-1 (GLP-1), GLP-1 analogue, exendin-2 or an exendin analogue with a spacer between the amino acid residues comparable to residues 7 and 8, or residues 8 and 9 of GLP-1, is new. The polypeptide comprises of any of 22 sequences having 28, 30, 33, 35, 37 or 39 amino acids fully defined in the specification.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following: (1) reducing neuronal death, promoting neuronal differentiation or proliferation, or promoting growth of neuronal processes, by contacting one or more neurons with the polypeptide; and (2) reducing formation or accumulation of amyloid protein by contacting one or more neurons with the polypeptide, which affects amyloid precursor protein metabolism.

BIOTECHNOLOGY - Preferred Polypeptide: The polypeptide is insulinotropic. The spacer is a 6-aminohexanoic acid spacer, which comprises less than four 6-aminohexanois acid residues. The polypeptide may further comprise any of 10 sequences having 30, 31, 39, 40, 43 or 46 amino acids fully defined in the specification. Preferred Method: The contacting cited in the methods of (2) is conducted in vivo or in vitro . Preparation: The peptides can be prepared using standard recombinant techniques.

ACTIVITY - Antidiabetic; Nootropic; Neuroprotective; Antiparkinsonian; Anticonvulsant; Cerebroprotective. Whole brain homogenates were assayed for amyloid-beta (Abeta) 1-40 levels following intracerebroventricular infusions of GLP-1, **exendin-4** , NGF or vehicle in normal control mice. After 48 hours, all animals were sacrificed, the brains removed and rapidly frozen in liquid nitrogen. Brains were pulverized and stored (-80degreesC) prior to assaying for Abeta levels. Equivalent volumes of conditioned media and whole brain homogenate were assayed for Abeta1-40 using a sandwich ELISA. The monoclonal antibody BAN50 (raised against Abeta1-16) was used as the capture antibody for species of Abeta (Abeta1-20 and Abeta1-42). All treatments reduced the levels of Abeta1-40 compared to vehicle. Multiple comparisons following significant main effects of treatment demonstrated that Abeta1-40 levels were reduced significantly following 6.6 mug GLP1 (36%, p less than 0.01) treatment.

MECHANISM OF ACTION - Insulinotropic; Insulin Agonist.

USE - The polypeptides are useful for treating a subject with diabetes (particularly type 2 diabetes) or a neurodegenerative condition (e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, stroke, multiple sclerosis, brain injury, spinal cord injury or peripheral neuropathy), as well as for reducing the symptom(s) of neurodegenerative conditions in a subject. The polypeptide is also useful for reducing neuronal death (which is caused by a neurodegenerative condition, a toxin or an injury), promoting neuronal differentiation or proliferation, promoting growth of neuronal processes, reducing formation or accumulation of amyloid protein. The polypeptides are also useful for treating a subject with neurotoxic injury or

neurodegenerative condition, or for reducing the symptom(s) of neurotoxic injury or neurodegenerative condition in a subject.

ADMINISTRATION - For in vivo use, the dosage is 0.1 pmoles/kg/minute to 100 nmoles/kg/minute for continuous administration; and 0.01-400 nmoles/kg for bolus injection. Administration is oral, intravenous, intramuscular, intraperitoneal, topical, transdermal, local, systemic, intraventricular, intracerebral, subdural or intrathecal.

EXAMPLE - The peptides were synthesized on a **PEG** -Polystyrene resin using Fmoc derivatives of amino acids. (119 pages)

L249 ANSWER 2 OF 9 USPATFULL
IN Piccariello, Thomas, Blacksburg, VA, UNITED STATES
Olon, Lawrence P., Bristol, TN, UNITED STATES
Kirk, Randal J., Radford, VA, UNITED STATES
TI Active agent delivery systems and methods for protecting and administering active agents
AB A composition comprising a polypeptide and an active agent covalently attached to the polypeptide. Also provided is a method for delivery of an active agent to a patient comprising administering to the patient a composition comprising a polypeptide and an active agent covalently attached to the polypeptide. Also provided is a method for protecting an active agent from degradation comprising covalently attaching the active agent to a polypeptide. Also provided is a method for controlling release of an active agent from a composition comprising covalently attaching the active agent to the polypeptide.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L249 ANSWER 3 OF 9 BIOTECHDS COPYRIGHT 2003 THOMSON DERWENT AND ISI
AU SHERIDAN S D
TI Inducing stem cell differentiation by treating isolated stem cells with a retinoid such that portion of stem cells differentiate into hepaticopancreatic tissue such as pancreatic tissue, pancreatic endocrine tissue;
diabetic servere combined immmunodeficiency mouse animal model for disease therapy and tissue engineering
AN 2003-09339 BIOTECHDS
AB DERWENT ABSTRACT:
NOVELTY - Inducing (M1) stem cell differentiation by treating isolated stem cells with a retinoid under conditions effective to cause at least a portion of the stem cells to differentiate into hepaticopancreatic tissue, is new.

DETAILED DESCRIPTION - An INDEPENDENT CLAIM is also included for a composition (I) comprising the hepaticopancreatic tissue produced by (M1).

BIOTECHNOLOGY - Preferred Method: The stem cells are obtained from a stem cell source chosen from placenta, bone marrow, adipose tissue, neural tissue, umbilical cord, blastocyst inner cell mass, and germ cells. The retinoid is vitamin A, retinol, retinal, or retinoic acid, preferably retinoic acid. The conditions are effective to differentiate at least 1, preferably 5 % of the stem cells into hepaticopancreatic tissue. The method further involves treating the isolated stem cells with a morphogen such as a member of the **glucagon**-like peptide family, a cAMP raising agent, nicotinamide, a transcription factor, a protein growth factor, or their mixtures. Preferably, the morphogen is chosen from **glucagon**-like peptide (GLP)-1, **exendin-4**, PDX-1, Ngn-3, gastrin, gastrin-releasing peptide, hepatocyte growth factor, betacellulin, or their mixtures. Preferred Composition: (I) comprises hepaticopancreatic tissue which comprises glucose-responsive insulin-producing cells. (I) comprises 1 % or more of the hepaticopancreatic tissue produced by (M1). Preferably (I) comprises 10 % or more of the hepaticopancreatic tissue, and is obtained by purifying the hepaticopancreatic tissue produced by (M1).

ACTIVITY - Antidiabetic; Antiinflammatory; Hepatotropic; Cytostatic. Insulin-producing cells produced by differentiation of embryonic stem

(ES) cells were cultured and were stained with the vital dye dithizone (DTZ). DTZ is a specific dye for zinc-containing granules that were especially abundant in differentiated beta-cells and were representative of insulin-containing storage structures. 200-300 DTZ positively stained cell clusters were transplanted under the kidney capsule of streptozotocin (STZ) induced diabetic serve combined immmunodeficient (SCID) mice to evaluate their ability to reverse the diabetic state of the animal. The results showed the ability of retinoic acid-treated differentiated embryonic stem cells to correct the blood glucose levels in STZ-SCID mice after transplantation.

MECHANISM OF ACTION - Cell therapy.

USE - (M1) is useful for inducing differentiation of stem cells (preferably mammalian embryonic stem cells) to hepaticopancreatic tissue such as pancreatic tissue; pancreatic endocrine tissue which comprises insulin-producing cells that are glucose-responsive; or liver tissue. (I) is useful for treating a mammal which involves identifying a mammal having an extraintestinal gastrointestinal disorder (a hepaticopancreatic disorder such as diabetes, pancreatitis, hepatic cirrhosis, hepatitis, cancer, and pancreatico-biliary disease) and administering (I) to the mammal. Preferably, (I) comprises glucose-responsive insulin-producing cells and is useful for treating diabetes in humans. (All claimed.)

ADMINISTRATION - (I) is preferably injected directly into the organ. No dosage is given.

EXAMPLE - Embryonic stem (ES) cell lines were cultured and spilt 1:8 every three days for 4 passages on gelatin coated tissue culture (TC) dishes without mouse embryonic fibroblasts (MEF's) (with 1500 units/ml lymphocyte inhibitory factor (LIF) in media) to remove MEF's from culture. The resulting stem cells were then differentiated as follows. On day 1, the stem cells were treated with trypsin to break up some aggregation and then suspended in 1 % fetal calf serum (FCS) media (without LIF). The stem cell were then allowed to self-aggregated into embryoid bodies in suspension culture. On day 3, the cells were given a fresh media change and then split among two bacterial petri dishes. A solution containing 1 micro-M retinoic acid was intermixed with the sample and both the control (no retinoic acid) and the sample were allowed to incubate at 37 degrees C. Fresh media were supplied at day 5 (with fresh 1 micro-M retinoic acid for the treated sample). At day 7 fresh media was supplied for both, with no retinoic acid (retinoic acid only present from days 3-7). Fresh media was supplied again on day 9. On day 11, the cells were again trypsinized and then placed into TC dishes with 10 % FCS media (no LIF). Small aliquots were taken at various times (days 14, 17, 19, 22 and 25) from the cultures and used for analysis by reverse transcriptase **polymerase** chain reaction (RT-PCR). On day 14, the media was changed for the two groups of cells, in each population (control and sample). On day 17, the media was changed again. On day 19, adherent cells were gently blown off, then trypsinized and resuspended in 10 % FCS in bacterial petri dish suspension cultures. On days 22 and 25, the remaining cells were collected, and a portion retained for RT-PCR analysis. All culturing from day 1 forward was performed in 25 millimolar (mM) glucose (high glucose) until after day 19, when it was changed to 5.5 mM glucose (lower glucose). Total RNA from each aliquot collected above was purified. The presence of specific RNA transcripts (i.e. insulin) was determined by RT-PCR. Total RNA was prepared from cultures of differentiating ES cells. RT-PCR analyses were performed. The RT-PCR results showed that no insulin was produced in any of the control samples, indicating an absence of insulin or amylase producing cells. In contrast, insulin-producing cells resulted when stem cells were treated with retinoic acid, as indicated by the presence of a correctly sized band during gel electrophoresis of insulin-specific RT-PCR generated products of RNA purified from aliquots obtained at days 14, 17, 19 and 22.(19 pages)

L249 ANSWER 4 OF 9 WPIDS (C) 2003 THOMSON DERWENT
IN PRICKETT, K; YOUNG, A
TI Modified exendin or an exendin agonist linked to one or more polyethylene

glycol (PEG) polymers, modulate plasma glucose levels, useful for treating disorders such as diabetes and obesity.

AN 2000-672834 [65] WPIDS

AB WO 200066629 A UPAB: 20001214

NOVELTY - A modified exendin (I) or exendin agonist (II) comprising (I) or (II) linked to one or more polyethylene glycol (PEG) polymers, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a method for making (I) or (II) comprising linking one or more PEG polymers to (I) and/or (II);

(2) a method for treating a disease benefited by administration of (I) or (II);

(3) a method of beneficially regulating gastrointestinal motility comprising administering (I) and/or (II);

(4) a method for treatment of ingestion of a toxin comprising administering (I) or (II) to prevent or reduce the passage of stomach contents to the intestines and aspirating the contents of the stomach;

(5) a method for reducing appetite or weight, lowering plasma lipids, treating diabetes mellitus, modulating triglyceride levels, or suppressing glucagon secretion comprising administering (I) and/or (II); and

(6) a pharmaceutical composition for use in the treatment of conditions or disorders associated with hypernutrition, or in reducing the appetite or weight of a subject, or in suppressing glucagon secretion, or in modulating triglyceride levels comprising administering (I) and/or (II).

ACTIVITY - Anorectic; antidiabetic; hyperglycemic; hypoglycemic.

No relevant biological data is given.

MECHANISM OF ACTION - Exendins modulate plasma glucose levels.

No relevant biological data is given.

USE - (I) and/or (II) are useful for treatment of diabetes and conditions that would be benefited by lowering plasma glucose or delaying and/or slowing gastric emptying or inhibiting food intake such as obesity and eating disorders.

Dwg.0/6

L249 ANSWER 5 OF 9 WPIDS (C) 2003 THOMSON DERWENT

IN GEDULIN, B; YOUNG, A

TI Lowering plasma glucagon using exendin, an exendin agonist, a modified exendin or a modified exendin agonist, useful for treating hyperglucagonemia and diabetes.

AN 2000-490999 [43] WPIDS

CR 2000-514584 [46]; 2001-514422 [56]

AB WO 200041548 A UPAB: 20021120

NOVELTY - A new method for lowering plasma glucagon comprises administering a compound (C1) selected from exendin, an exendin agonist, a modified exendin or a modified exendin agonist.

ACTIVITY - Antidiabetic; dermatological.

MECHANISM OF ACTION - The compounds lower plasma glucagon level.

The safety, tolerability, and efficacy of synthetic **exendin -4** was evaluated in 8 male non-insulin using patients with type 2 diabetes who had discontinued other antidiabetic therapy for a minimum of 7 days. Each patient received subcutaneous (SC) injections of placebo (PBO) and 0.1, 0.2, and 0.3 micro g/kg **exendin-4** 48 hours apart in a single-blind, dose-rising, placebo controlled crossover design. Five patients also received a 0.4 micro g/kg dose. Plasma glucose, insulin and **glucagon** concentrations were assessed during fasting and in response to a 7 Kcal/kg Sustacal (RTM) challenge administered at the time of **exendin-4**/PBO injection. Gastric emptying was evaluated by measuring serum acetaminophen concentrations following a 20 mg/kg oral dose of liquid acetaminophen administered with the Sustacal (RTM).

No safety issues were identified based upon reported adverse events, EKG (undefined) and safety lab monitoring. Doses of 0.3 and 0.4 micro g/kg elicited a dose-dependent increase in nausea. Vomiting occurred at the highest dose.

Plasma glucose concentrations were reduced in all doses of **exendin-4** compared to PBO although insulin concentrations were not significantly different. The 8 hour mean plus or minus SE changes in plasma glucose AUC (undefined) from baseline were +391 plus or minus 187, -263 plus or minus 108, -247 plus or minus 64, -336 plus or minus 139, and -328 plus or minus 70 (mg)(hr)/dL for the PBO, 0.1, 0.2, 0.3, and 0.4 micro g/kg doses respectively. The 3 hour changes in plasma **glucagon** were +128.0 plus or minus 19.2, -5.6 plus or minus 10.5, -29.4 plus or minus 18.6, -40.5 plus or minus 24.5, and +6.9 plus or minus 38.6 (pg)(hr)/mL respectively. The gastric emptying rate was slowed in all doses and the mean total absorbed acetaminophen over 6 hours was reduced by 51%, 50%, 57% and 79% compared to PBO for 0.1, 0.2, 0.3, and 0.4 micro g/kg doses respectively.

In summary, SC injection of **exendin-4** to patients identified no safety issues, was tolerated at doses at most 0.3 micro g/kg, reduced plasma glucose and **glucagon** and slowed the rate of gastric emptying.

USE - The method is useful for lowering plasma glucagon in subjects, preferably humans, suffering from necrolytic erythema or glucagonoma (claimed). The method is also useful for treating hyperglucagonemia and other conditions that would benefit from reduced glucagon levels and/or suppression of glucagon, e.g. type 1 and type 2 diabetes.
Dwg.0/6

L249 ANSWER 6 OF 9 DRUGU COPYRIGHT 2003 THOMSON DERWENT
SO Exp.Clin.Endocrinol.Diabetes (107, Suppl. 3, S108-S113, 1999) 2 Fig. 38 Ref.
CODEN: ECEDF ISSN: 0947-7349
AV Diabetes-Schulungszentrum, Medizinische Klinik I, Klinikum der Johann Wolfgang Goethe-Universitaet, Theodor-Stern-Kai 7, D- 60590 Frankfurt am Main, Germany. (e-mail: DSZ-Haak@em.uni- frankfurt.de).
AU Haak
TI New developments in the treatment of type 1 diabetes mellitus.
AN 1999-43452 DRUGU T E
AB New developments in the treatment of type 1 diabetes mellitus are reviewed. Insulin delivery, Pseudomassaria induced reversal of clinical signs of diabetes mellitus in mice, studies with insulin analogs (protracted- and fast-acting), glucagon-like peptides and blood glucose monitoring systems are discussed. (conference paper: International Symposium on Autoimmunity and Endocrinology, Frankfurt, Germany, 1999).
ABEX Intrapulmonary insulin delivery has become feasible as a result of the development of high-efficacy nebulizers which provide a sufficient degree of intrapulmonary drug retention. This method of insulin administration has proved safe and efficient in clinical studies. P.o. insulin delivery seems feasible when surface active substances such as bile salts are used as resorption enhancers to cross the mucosal membrane in the gut. Use of zona occludens toxin (produced by Vibrio cholerae) has been reported. Protease inhibitors and **polymer** coatings have been used to protect the insulin molecule against digestive proteolytic activity. Pseudomassaria (L-783281) reverses the clinical signs of diabetes mellitus in mice by binding to the inner part of the insulin receptor and inducing typical insulin effects. Various insulin analogs have been designed and tested for clinical use including long-acting analogs such as HOE 901 and NN 304 and fast-acting lispro and insulin aspart (aimed at improving postprandial glucose regulation). **Glucagon**-like peptide-1 (GLP-1) improves metabolic control by a variety of effects but has a very short half-life. Derivatives with better resistance to degradation have been developed (**exendin-4**). Other approaches include the development of substances which augment endogenous release of GLP-1 and use of valine pyrrolidide to improve glucose tolerance. Various approaches aimed at improving or easing blood glucose self-monitoring have been developed. (E27/SK)

L249 ANSWER 7 OF 9 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 1
SO Journal of Biological Chemistry, (April 17, 1998) Vol. 273, No. 16, pp.

9778-9784.
ISSN: 0021-9258.
AU Pohl, Markus; Wank, Stephen A. (1)
TI Molecular cloning of the helodermin and **exendin-4** cDNAs in the lizard: Relationship to vasoactive intestinal polypeptide/pituitary adenylate cyclase activating polypeptide and **glucagon**-like peptide 1 and evidence against the existence of mammalian homologues.
AB Helodermin and **exendin-4**, two peptides isolated from the salivary gland of the Gila monster, Heloderma suspectum, are approximately 50% homologous to vasoactive intestinal peptide (VIP) and **glucagon**-like peptide-1 (GLP-1), respectively, and interact with the mammalian receptors for VIP and GLP-1 with equal or higher affinity and efficacy. Immunohistochemical studies suggested the presence of helodermin-like peptides in mammals. To determine whether helodermin and **exendin-4** are present in mammals and their evolutionary relationship to VIP and GLP-1, their cDNAs were first cloned from Gila monster salivary gland. Northern blots and reverse transcription-**polymerase** chain reaction of multiple Gila monster tissues identified apprx500-base pair transcripts only from salivary gland. Both helodermin and **exendin-4** full-length cDNAs were apprx500 base pairs long, and they encoded precursor proteins containing the entire amino acid sequence of helodermin and **exendin-4**, as well as a 44- or 45-amino acid N-terminal extension peptide, respectively, having apprx60% homology. The size and structural organization of these cDNAs indicated that they were closely related to one another but markedly different from known cDNAs for the VIP/GLP-1 peptide family previously identified in both lower and higher evolved species. Cloning of the Gila monster VIP/peptide histidine isoleucine, pituitary adenylate cyclase activating polypeptide, and **glucagon** / GLP-1 cDNAs and Southern blotting of Gila monster DNA demonstrate the coexistence of separate genes for these peptides and suggests, along with the restricted salivary gland expression, that helodermin and **exendin-4** coevolved to serve a separate specialized function. Probing of a variety of rat and human tissues on Northern blots, human and rat Southern blots, and genomic and cDNA libraries with either helodermin- or **exendin-4**-specific cDNAs failed to identify evidence for mammalian homologues. These data indicate that helodermin and **exendin-4** are not the precursors to VIP and GLP-1 and that they belong to a separate peptide family encoded by separate genes. Furthermore, the existence of as yet undiscovered mammalian homologues to helodermin and **exendin-4** seems unlikely.

L249 ANSWER 8 OF 9 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 2
SO Journal of Biological Chemistry, (1997) Vol. 272, No. 7, pp. 4108-4115.
ISSN: 0021-9258.
AU Chen, Yuqing E.; Drucker, Daniel J. (1)
TI Tissue-specific expression of unique mRNAs that encode proglucagon-derived peptides or exendin 4 in the lizard.
AB **Glucagon**-like peptide 1 stimulates insulin secretion and inhibits **glucagon** secretion, gastric emptying, and feeding, suggesting it may be biologically useful for the treatment of diabetes. A lizard **glucagon**-like peptide 1 (GLP-1)-related peptide, **exendin 4**, binds to the GLP-1 receptor and mimics the actions of GLP-1 in vivo. To determine the genetic relationship between **exendin 4** and GLP-1, we analyzed the structure and expression of pancreatic and intestinal proglucagon mRNAs in the reptile Heloderma suspectum. Two different proglucagon cDNAs (lizard proglucagon I (LPI) and lizard proglucagon 11 (LPII)), with unique 3'-untranslated regions were identified. Two LPI mRNA transcripts, apprx 1.6 and 2.1 kilobases, encoded **glucagon** and GLP-1 but not GLP-2 and were restricted in expression to the pancreas. In contrast, a 1.1-kilobase LPII mRNA transcript, encoding **glucagon**, GLP-1, and GLP-2 utilized a different 3'-untranslated region and was expressed in both pancreas and

intestine. Lizard proglucagon mRNA transcripts were not detectable by reverse transcription-**polymerase** chain reaction or Northern blotting in salivary gland. A single class of lizard salivary gland proexendin cDNAs encoded the sequence of **exendin 4** and a 45-amino acid exendin NH-2-terminal peptide. Exendin mRNA transcripts were expressed in the salivary gland, but not pancreas or intestine. These data demonstrate that GLP-1 and **exendin 4** represent related yet distinct peptides encoded by different genes in the lizard.

L249 ANSWER 9 OF 9 ADISINSIGHT COPYRIGHT (C) 2003 Adis Data Information BV
SO Adis R&D Insight

=> d l249 1-9 so ti au abs ibib

L249 ANSWER 1 OF 9 BIOTECHDS COPYRIGHT 2003 THOMSON DERWENT AND ISI
TI New Glucagon-like peptide-1 or exendin-2 polypeptides, or their analogues, useful for treating a subject with diabetes or a neurodegenerative condition (e.g. Alzheimer's disease, stroke, multiple sclerosis or brain injury);
recombinant glucagon-like protein preparation for disease therapy
AU GREIG N H; EGAN J; DOYLE M; HOLLOWAY H; PERRY T A
AN 2003-12947 BIOTECHDS
AB DERWENT ABSTRACT:
NOVELTY - A purified polypeptide, which comprises the amino acid sequence of **Glucagon**-like peptide-1 (GLP-1), GLP-1 analogue, exendin-2 or an exendin analogue with a spacer between the amino acid residues comparable to residues 7 and 8, or residues 8 and 9 of GLP-1, is new. The polypeptide comprises of any of 22 sequences having 28, 30, 33, 35, 37 or 39 amino acids fully defined in the specification.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following: (1) reducing neuronal death, promoting neuronal differentiation or proliferation, or promoting growth of neuronal processes, by contacting one or more neurons with the polypeptide; and (2) reducing formation or accumulation of amyloid protein by contacting one or more neurons with the polypeptide, which affects amyloid precursor protein metabolism.

BIOTECHNOLOGY - Preferred Polypeptide: The polypeptide is insulinotropic. The spacer is a 6-aminohexanoic acid spacer, which comprises less than four 6-aminohexanois acid residues. The polypeptide may further comprise any of 10 sequences having 30, 31, 39, 40, 43 or 46 amino acids fully defined in the specification. Preferred Method: The contacting cited in the methods of (2) is conducted in vivo or in vitro . Preparation: The peptides can be prepared using standard recombinant techniques.

ACTIVITY - Antidiabetic; Nootropic; Neuroprotective; Antiparkinsonian; Anticonvulsant; Cerebroprotective. Whole brain homogenates were assayed for amyloid-beta (Abeta) 1-40 levels following intracerebroventricular infusions of GLP-1, **exendin-4** , NGF or vehicle in normal control mice. After 48 hours, all animals were sacrificed, the brains removed and rapidly frozen in liquid nitrogen. Brains were pulverized and stored (-80degreesC) prior to assaying for Abeta levels. Equivalent volumes of conditioned media and whole brain homogenate were assayed for Abeta1-40 using a sandwich ELISA. The monoclonal antibody BAN50 (raised against Abeta1-16) was used as the capture antibody for species of Abeta (Abeta1-20 and Abeta1-42). All treatments reduced the levels of Abeta1-40 compared to vehicle. Multiple comparisons following significant main effects of treatment demonstrated that Abeta1-40 levels were reduced significantly following 6.6 mug GLP1 (36%, p less than 0.01) treatment.

MECHANISM OF ACTION - Insulinotropic; Insulin Agonist.

USE - The polypeptides are useful for treating a subject with diabetes (particularly type 2 diabetes) or a neurodegenerative condition (e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, stroke, multiple sclerosis, brain injury,

spinal cord injury or peripheral neuropathy), as well as for reducing the symptom(s) of neurodegenerative conditions in a subject. The polypeptide is also useful for reducing neuronal death (which is caused by a neurodegenerative condition, a toxin or an injury), promoting neuronal differentiation or proliferation, promoting growth of neuronal processes, reducing formation or accumulation of amyloid protein. The polypeptides are also useful for treating a subject with neurotoxic injury or neurodegenerative condition, or for reducing the symptom(s) of neurotoxic injury or neurodegenerative condition in a subject.

ADMINISTRATION - For in vivo use, the dosage is 0.1 pmoles/kg/minute to 100 nmoles/kg/minute for continuous administration; and 0.01-400 nmoles/kg for bolus injection. Administration is oral, intravenous, intramuscular, intraperitoneal, topical, transdermal, local, systemic, intraventricular, intracerebral, subdural or intrathecal.

EXAMPLE - The peptides were synthesized on a **PEG** -Polystyrene resin using Fmoc derivatives of amino acids. (119 pages)

ACCESSION NUMBER: 2003-12947 BIOTECHDS
TITLE: New Glucagon-like peptide-1 or exendin-2 polypeptides, or their analogues, useful for treating a subject with diabetes or a neurodegenerative condition (e.g. Alzheimer's disease, stroke, multiple sclerosis or brain injury); recombinant glucagon-like protein preparation for disease therapy
AUTHOR: GREIG N H; EGAN J; DOYLE M; HOLLOWAY H; PERRY T A
PATENT ASSIGNEE: US DEPT HEALTH and HUMAN SERVICES
PATENT INFO: WO 20030011892 13 Feb 2003
APPLICATION INFO: WO 2002-US24141 30 Jul 2002
PRIORITY INFO: US 2001-309076 31 Jul 2001; US 2001-309076 31 Jul 2001
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 2003-268106 [26]

L249 ANSWER 2 OF 9 USPATFULL
TI Active agent delivery systems and methods for protecting and administering active agents
IN Piccariello, Thomas, Blacksburg, VA, UNITED STATES
Olon, Lawrence P., Bristol, TN, UNITED STATES
Kirk, Randal J., Radford, VA, UNITED STATES
AB A composition comprising a polypeptide and an active agent covalently attached to the polypeptide. Also provided is a method for delivery of an active agent to a patient comprising administering to the patient a composition comprising a polypeptide and an active agent covalently attached to the polypeptide. Also provided is a method for protecting an active agent from degradation comprising covalently attaching the active agent to a polypeptide. Also provided is a method for controlling release of an active agent from a composition comprising covalently attaching the active agent to the polypeptide.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2002:186092 USPATFULL
TITLE: Active agent delivery systems and methods for protecting and administering active agents
INVENTOR(S): Piccariello, Thomas, Blacksburg, VA, UNITED STATES
Olon, Lawrence P., Bristol, TN, UNITED STATES
Kirk, Randal J., Radford, VA, UNITED STATES

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2002099013	A1	20020725	
APPLICATION INFO.:	US 2001-933708	A1	20010822	(9)

	NUMBER	DATE	
PRIORITY INFORMATION:	US 2001-274622P	20010308	(60)
	US 2000-247621P	20001114	(60)

US 2000-247620P	20001114	(60)
US 2000-247595P	20001114	(60)
US 2000-247594P	20001114	(60)
US 2000-247635P	20001114	(60)
US 2000-247634P	20001114	(60)
US 2000-247606P	20001114	(60)
US 2000-247607P	20001114	(60)
US 2000-247608P	20001114	(60)
US 2000-247609P	20001114	(60)
US 2000-247610P	20001114	(60)
US 2000-247611P	20001114	(60)
US 2000-247702P	20001114	(60)
US 2000-247701P	20001114	(60)
US 2000-247700P	20001114	(60)
US 2000-247699P	20001114	(60)
US 2000-247698P	20001114	(60)
US 2000-247807P	20001114	(60)
US 2000-247833P	20001114	(60)
US 2000-247832P	20001114	(60)
US 2000-247927P	20001114	(60)
US 2000-247926P	20001114	(60)
US 2000-247930P	20001114	(60)
US 2000-247929P	20001114	(60)
US 2000-247928P	20001114	(60)
US 2000-247797P	20001114	(60)
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US 2000-247804P	20001114	(60)
US 2000-247803P	20001114	(60)
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US 2000-247561P	20001114	(60)
US 2000-247560P	20001114	(60)
US 2000-247559P	20001114	(60)
US 2000-247558P	20001114	(60)
US 2000-247556P	20001114	(60)
US 2000-247612P	20001114	(60)
US 2000-247613P	20001114	(60)
US 2000-247614P	20001114	(60)
US 2000-247615P	20001114	(60)
US 2000-247616P	20001114	(60)
US 2000-247617P	20001114	(60)
US 2000-247633P	20001114	(60)
US 2000-247632P	20001114	(60)
US 2000-247631P	20001114	(60)
US 2000-247630P	20001114	(60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: Robert M. Schulman, Esq., Hunton & Williams, Suite 1200, 1900 K Street, N.W., Washington, DC, 20006-1100
NUMBER OF CLAIMS: 40
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 8 Drawing Page(s)
LINE COUNT: 2048
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L249 ANSWER 3 OF 9 BIOTECHDS COPYRIGHT 2003 THOMSON DERWENT AND ISI
TI Inducing stem cell differentiation by treating isolated stem cells with a retinoid such that portion of stem cells differentiate into hepaticopancreatic tissue such as pancreatic tissue, pancreatic endocrine tissue;
diabetic servere combined immmunodeficiency mouse animal model for disease therapy and tissue engineering

AU SHERIDAN S D
AN 2003-09339 BIOTECHDS
AB DERWENT ABSTRACT:
NOVELTY - Inducing (M1) stem cell differentiation by treating isolated stem cells with a retinoid under conditions effective to cause at least a portion of the stem cells to differentiate into hepaticopancreatic tissue, is new.

DETAILED DESCRIPTION - An INDEPENDENT CLAIM is also included for a composition (I) comprising the hepaticopancreatic tissue produced by (M1).

BIOTECHNOLOGY - Preferred Method: The stem cells are obtained from a stem cell source chosen from placenta, bone marrow, adipose tissue, neural tissue, umbilical cord, blastocyst inner cell mass, and germ cells. The retinoid is vitamin A, retinol, retinal, or retinoic acid, preferably retinoic acid. The conditions are effective to differentiate at least 1, preferably 5 % of the stem cells into hepaticopancreatic tissue. The method further involves treating the isolated stem cells with a morphogen such as a member of the **glucagon**-like peptide family, a cAMP raising agent, nicotinamide, a transcription factor, a protein growth factor, or their mixtures. Preferably, the morphogen is chosen from **glucagon**-like peptide (GLP)-1, **exendin-4**, PDX-1, Ngn-3, gastrin, gastrin-releasing peptide, hepatocyte growth factor, betacellulin, or their mixtures. Preferred Composition: (I) comprises hepaticopancreatic tissue which comprises glucose-responsive insulin-producing cells. (I) comprises 1 % or more of the hepaticopancreatic tissue produced by (M1). Preferably (I) comprises 10 % or more of the hepaticopancreatic tissue, and is obtained by purifying the hepaticopancreatic tissue produced by (M1).

ACTIVITY - Antidiabetic; Antiinflammatory; Hepatotropic; Cytostatic. Insulin-producing cells produced by differentiation of embryonic stem (ES) cells were cultured and were stained with the vital dye dithizone (DTZ). DTZ is a specific dye for zinc-containing granules that were especially abundant in differentiated beta-cells and were representative of insulin-containing storage structures. 200-300 DTZ positively stained cell clusters were transplanted under the kidney capsule of streptozotocin (STZ) induced diabetic serve combined immmunodeficient (SCID) mice to evaluate their ability to reverse the diabetic state of the animal. The results showed the ability of retinoic acid-treated differentiated embryonic stem cells to correct the blood glucose levels in STZ-SCID mice after transplantation.

MECHANISM OF ACTION - Cell therapy.

USE - (M1) is useful for inducing differentiation of stem cells (preferably mammalian embryonic stem cells) to hepaticopancreatic tissue such as pancreatic tissue; pancreatic endocrine tissue which comprises insulin-producing cells that are glucose-responsive; or liver tissue. (I) is useful for treating a mammal which involves identifying a mammal having an extraintestinal gastrointestinal disorder (a hepaticopancreatic disorder such as diabetes, pancreatitis, hepatic cirrhosis, hepatitis, cancer, and pancreatico-biliary disease) and administering (I) to the mammal. Preferably, (I) comprises glucose-responsive insulin-producing cells and is useful for treating diabetes in humans. (All claimed.)

ADMINISTRATION - (I) is preferably injected directly into the organ. No dosage is given.

EXAMPLE - Embryonic stem (ES) cell lines were cultured and spilt 1:8 every three days for 4 passages on gelatin coated tissue culture (TC) dishes without mouse embryonic fibroblasts (MEF's) (with 1500 units/ml lymphocyte inhibitory factor (LIF) in media) to remove MEF's from culture. The resulting stem cells were then differentiated as follows. On day 1, the stem cells were treated with trypsin to break up some aggregation and then suspended in 1 % fetal calf serum (FCS) media (without LIF). The stem cell were then allowed to self-aggregated into embryoid bodies in suspension culture. On day 3, the cells were given a fresh media change and then split among two bacterial petri dishes. A solution containing 1 micro-M retinoic acid was intermixed with the sample and both the control (no retinoic acid) and the sample were

allowed to incubate at 37 degrees C. Fresh media were supplied at day 5 (with fresh 1 micro-M retinoic acid for the treated sample). At day 7 fresh media was supplied for both, with no retinoic acid (retinoic acid only present from days 3-7). Fresh media was supplied again on day 9. On day 11, the cells were again trypsinized and then placed into TC dishes with 10 % FCS media (no LIF). Small aliquots were taken at various times (days 14, 17, 19, 22 and 25) from the cultures and used for analysis by reverse transcriptase **polymerase** chain reaction (RT-PCR). On day 14, the media was changed for the two groups of cells, in each population (control and sample). On day 17, the media was changed again. On day 19, adherent cells were gently blown off, then trypsinized and resuspended in 10 % FCS in bacterial petri dish suspension cultures. On days 22 and 25, the remaining cells were collected, and a portion retained for RT-PCR analysis. All culturing from day 1 forward was performed in 25 millimolar (mM) glucose (high glucose) until after day 19, when it was changed to 5.5 mM glucose (lower glucose). Total RNA from each aliquot collected above was purified. The presence of specific RNA transcripts (i.e. insulin) was determined by RT-PCR. Total RNA was prepared from cultures of differentiating ES cells. RT-PCR analyses were performed. The RT-PCR results showed that no insulin was produced in any of the control samples, indicating an absence of insulin or amylase producing cells. In contrast, insulin-producing cells resulted when stem cells were treated with retinoic acid, as indicated by the presence of a correctly sized band during gel electrophoresis of insulin-specific RT-PCR generated products of RNA purified from aliquots obtained at days 14, 17, 19 and 22.(19 pages)

ACCESSION NUMBER: 2003-09339 BIOTECHDS
TITLE: Inducing stem cell differentiation by treating isolated stem cells with a retinoid such that portion of stem cells differentiate into hepaticopancreatic tissue such as pancreatic tissue, pancreatic endocrine tissue; diabetic servere combined immmunodeficiency mouse animal model for disease therapy and tissue engineering
AUTHOR: SHERIDAN S D
PATENT ASSIGNEE: CYTHERA INC
PATENT INFO: WO 2002096203 5 Dec 2002
APPLICATION INFO: WO 2002-US16830 23 May 2002
PRIORITY INFO: US 2001-293582 25 May 2001; US 2001-293582 25 May 2001
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 2003-140401 [13]

L249 ANSWER 4 OF 9 WPIDS (C) 2003 THOMSON DERWENT
TI Modified exendin or an exendin agonist linked to one or more polyethylene glycol (PEG) polymers, modulate plasma glucose levels, useful for treating disorders such as diabetes and obesity.
IN PRICKETT, K; YOUNG, A
AN 2000-672834 [65] WPIDS
AB WO 200066629 A UPAB: 20001214
NOVELTY - A modified exendin (I) or exendin agonist (II) comprising (I) or (II) linked to one or more polyethylene glycol (PEG) polymers, is new.
DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:
(1) a method for making (I) or (II) comprising linking one or more PEG polymers to (I) and/or (II);
(2) a method for treating a disease benefited by administration of (I) or (II);
(3) a method of beneficially regulating gastrointestinal motility comprising administering (I) and/or (II);
(4) a method for treatment of ingestion of a toxin comprising administering (I) or (II) to prevent or reduce the passage of stomach contents to the intestines and aspirating the contents of the stomach;
(5) a method for reducing appetite or weight, lowering plasma lipids, treating diabetes mellitus, modulating triglyceride levels, or suppressing glucagon secretion comprising administering (I) and/or (II); and

(6) a pharmaceutical composition for use in the treatment of conditions or disorders associated with hypernutrition, or in reducing the appetite or weight of a subject, or in suppressing glucagon secretion, or in modulating triglyceride levels comprising administering (I) and/or (II).

ACTIVITY - Anorectic; antidiabetic; hyperglycemic; hypoglycemic.

No relevant biological data is given.

MECHANISM OF ACTION - Exendins modulate plasma glucose levels.

No relevant biological data is given.

USE - (I) and/or (II) are useful for treatment of diabetes and conditions that would be benefited by lowering plasma glucose or delaying and/or slowing gastric emptying or inhibiting food intake such as obesity and eating disorders.

Dwg.0/6

ACCESSION NUMBER: 2000-672834 [65] WPIDS
DOC. NO. CPI: C2000-203847
TITLE: Modified exendin or an exendin agonist linked to one or more polyethylene glycol (PEG) polymers, modulate plasma glucose levels, useful for treating disorders such as diabetes and obesity.
DERWENT CLASS: A96 B04
INVENTOR(S): PRICKETT, K; YOUNG, A
PATENT ASSIGNEE(S): (AMYL-N) AMYLIN PHARM INC
COUNTRY COUNT: 90
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000066629	A1	20001109	(200065)*	EN	113
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ TZ UG ZW					
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW					
AU 2000046883	A	20001117	(200111)		
BR 2000010705	A	20020205	(200213)		
EP 1175443	A1	20020130	(200216)	EN	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI					
CN 1372570	A	20021002	(200307)		
JP 2002544127	W	20021224	(200313)		146

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000066629	A1	WO 2000-US11814	20000428
AU 2000046883	A	AU 2000-46883	20000428
BR 2000010705	A	BR 2000-10705	20000428
		WO 2000-US11814	20000428
EP 1175443	A1	EP 2000-928685	20000428
		WO 2000-US11814	20000428
CN 1372570	A	CN 2000-809516	20000428
JP 2002544127	W	JP 2000-615657	20000428
		WO 2000-US11814	20000428

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2000046883	A	Based on	WO 200066629
BR 2000010705	A	Based on	WO 200066629
EP 1175443	A1	Based on	WO 200066629
JP 2002544127	W	Based on	WO 200066629

PRIORITY APPLN. INFO: US 1999-132018P 19990430

L249 ANSWER 5 OF 9 WPIDS (C) 2003 THOMSON DERWENT
TI Lowering plasma glucagon using exendin, an exendin agonist, a modified exendin or a modified exendin agonist, useful for treating hyperglucagonemia and diabetes.
IN GEDULIN, B; YOUNG, A
AN 2000-490999 [43] WPIDS
CR 2000-514584 [46]; 2001-514422 [56]
AB WO 200041548 A UPAB: 20021120
NOVELTY - A new method for lowering plasma glucagon comprises administering a compound (C1) selected from exendin, an exendin agonist, a modified exendin or a modified exendin agonist.

ACTIVITY - Antidiabetic; dermatological.

MECHANISM OF ACTION - The compounds lower plasma glucagon level.

The safety, tolerability, and efficacy of synthetic **exendin -4** was evaluated in 8 male non-insulin using patients with type 2 diabetes who had discontinued other antidiabetic therapy for a minimum of 7 days. Each patient received subcutaneous (SC) injections of placebo (PBO) and 0.1, 0.2, and 0.3 micro g/kg **exendin-4** 48 hours apart in a single-blind, dose-rising, placebo controlled crossover design. Five patients also received a 0.4 micro g/kg dose. Plasma glucose, insulin and **glucagon** concentrations were assessed during fasting and in response to a 7 Kcal/kg Sustacal (RTM) challenge administered at the time of **exendin-4**/PBO injection. Gastric emptying was evaluated by measuring serum acetaminophen concentrations following a 20 mg/kg oral dose of liquid acetaminophen administered with the Sustacal (RTM).

No safety issues were identified based upon reported adverse events, EKG (undefined) and safety lab monitoring. Doses of 0.3 and 0.4 micro g/kg elicited a dose-dependent increase in nausea. Vomiting occurred at the highest dose.

Plasma glucose concentrations were reduced in all doses of **exendin-4** compared to PBO although insulin concentrations were not significantly different. The 8 hour mean plus or minus SE changes in plasma glucose AUC (undefined) from baseline were +391 plus or minus 187, -263 plus or minus 108, -247 plus or minus 64, -336 plus or minus 139, and -328 plus or minus 70 (mg)(hr)/dL for the PBO, 0.1, 0.2, 0.3, and 0.4 micro g/kg doses respectively. The 3 hour changes in plasma **glucagon** were +128.0 plus or minus 19.2, -5.6 plus or minus 10.5, -29.4 plus or minus 18.6, -40.5 plus or minus 24.5, and +6.9 plus or minus 38.6 (pg)(hr)/mL respectively. The gastric emptying rate was slowed in all doses and the mean total absorbed acetaminophen over 6 hours was reduced by 51%, 50%, 57% and 79% compared to PBO for 0.1, 0.2, 0.3, and 0.4 micro g/kg doses respectively.

In summary, SC injection of **exendin-4** to patients identified no safety issues, was tolerated at doses at most 0.3 micro g/kg, reduced plasma glucose and **glucagon** and slowed the rate of gastric emptying.

USE - The method is useful for lowering plasma glucagon in subjects, preferably humans, suffering from necrolytic erythema or glucagonoma (claimed). The method is also useful for treating hyperglucagonemia and other conditions that would benefit from reduced glucagon levels and/or suppression of glucagon, e.g. type 1 and type 2 diabetes.

Dwg.0/6

ACCESSION NUMBER: 2000-490999 [43] WPIDS
CROSS REFERENCE: 2000-514584 [46]; 2001-514422 [56]
DOC. NO. CPI: C2000-147547
TITLE: Lowering plasma glucagon using exendin, an exendin agonist, a modified exendin or a modified exendin agonist, useful for treating hyperglucagonemia and diabetes.
DERWENT CLASS: A25 A96 B04
INVENTOR(S): GEDULIN, B; YOUNG, A

PATENT ASSIGNEE(S): (AMYL-N) AMYLIN PHARM INC
COUNTRY COUNT: 91
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000041548	A2	20000720	(200043)*	EN	96
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ TZ UG ZW					
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
AU 2000024136	A	20000801	(200054)		
NO 2001003469	A	20010914	(200163)		
EP 1143989	A2	20011017	(200169)	EN	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI					
BR 2000007823	A	20011120	(200202)		
KR 2001086165	A	20010908	(200219)		
KR 2002001719	A	20020109	(200246)		
CN 1347327	A	20020501	(200252)		
JP 2002538084	W	20021112	(200275)		104

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000041548	A2	WO 2000-US942	20000114
AU 2000024136	A	AU 2000-24136	20000114
NO 2001003469	A	WO 2000-US942	20000114
		NO 2001-3469	20010712
EP 1143989	A2	EP 2000-902415	20000114
		WO 2000-US942	20000114
BR 2000007823	A	BR 2000-7823	20000114
		WO 2000-US942	20000114
KR 2001086165	A	KR 2001-708904	20010713
KR 2002001719	A	WO 2000-US942	20000114
		KR 2001-708892	20010713
CN 1347327	A	CN 2000-805017	20000114
JP 2002538084	W	JP 2000-593169	20000114
		WO 2000-US942	20000114

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2000024136	A	Based on	WO 200041548
EP 1143989	A2	Based on	WO 200041548
BR 2000007823	A	Based on	WO 200041548
KR 2002001719	A	Based on	WO 200041548
JP 2002538084	W	Based on	WO 200041548

PRIORITY APPLN. INFO: US 2000-175365P 20000110; US 1999-116380P 19990114; US 1999-132017P 19990430

L249 ANSWER 6 OF 9 DRUGU COPYRIGHT 2003 THOMSON DERWENT
SO Exp.Clin.Endocrinol.Diabetes (107, Suppl. 3, S108-S113, 1999) 2 Fig. 38 Ref.
CODEN: ECEDF ISSN: 0947-7349
AV Diabetes-Schulungszentrum, Medizinische Klinik I, Klinikum der Johann Wolfgang Goethe-Universitaet, Theodor-Stern-Kai 7, D- 60590 Frankfurt am Main, Germany. (e-mail: DSZ-Haak@em.uni- frankfurt.de).
TI New developments in the treatment of type 1 diabetes mellitus.
AU Haak

AN 1999-43452 DRUGU T E
AB New developments in the treatment of type 1 diabetes mellitus are reviewed. Insulin delivery, Pseudomassaria induced reversal of clinical signs of diabetes mellitus in mice, studies with insulin analogs (protracted- and fast-acting), glucagon-like peptides and blood glucose monitoring systems are discussed. (conference paper: International Symposium on Autoimmunity and Endocrinology, Frankfurt, Germany, 1999).
ABEX Intrapulmonary insulin delivery has become feasible as a result of the development of high-efficacy nebulizers which provide a sufficient degree of intrapulmonary drug retention. This method of insulin administration has proved safe and efficient in clinical studies. P.o. insulin delivery seems feasible when surface active substances such as bile salts are used as resorption enhancers to cross the mucosal membrane in the gut. Use of zona occludens toxin (produced by Vibrio cholerae) has been reported. Protease inhibitors and **polymer** coatings have been used to protect the insulin molecule against digestive proteolytic activity. Pseudomassaria (L-783281) reverses the clinical signs of diabetes mellitus in mice by binding to the inner part of the insulin receptor and inducing typical insulin effects. Various insulin analogs have been designed and tested for clinical use including long-acting analogs such as HOE 901 and NN 304 and fast-acting lispro and insulin aspart (aimed at improving postprandial glucose regulation). **Glucagon**-like peptide-1 (GLP-1) improves metabolic control by a variety of effects but has a very short half-life. Derivatives with better resistance to degradation have been developed (**exendin-4**). Other approaches include the development of substances which augment endogenous release of GLP-1 and use of valine pyrrolidide to improve glucose tolerance. Various approaches aimed at improving or easing blood glucose self-monitoring have been developed. (E27/SK)
ACCESSION NUMBER: 1999-43452 DRUGU T E
TITLE: New developments in the treatment of type 1 diabetes mellitus.
AUTHOR: Haak
CORPORATE SOURCE: Univ.Frankfurt
LOCATION: Frankfurt, Ger.
SOURCE: Exp.Clin.Endocrinol.Diabetes (107, Suppl. 3, S108-S113, 1999)
2 Fig. 38 Ref.
CODEN: ECEDF ISSN: 0947-7349
AVAIL. OF DOC.: Diabetes-Schulungszentrum, Medizinische Klinik I, Klinikum der Johann Wolfgang Goethe-Universitaet, Theodor-Stern-Kai 7, D- 60590 Frankfurt am Main, Germany. (e-mail: DSZ-Haak@em.uni- frankfurt.de).
LANGUAGE: English
DOCUMENT TYPE: Journal
FIELD AVAIL.: AB; LA; CT
FILE SEGMENT: Literature

L249 ANSWER 7 OF 9 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 1
SO Journal of Biological Chemistry, (April 17, 1998) Vol. 273, No. 16, pp. 9778-9784.
ISSN: 0021-9258.
TI Molecular cloning of the helodermin and **exendin-4** cDNAs in the lizard: Relationship to vasoactive intestinal polypeptide/pituitary adenylate cyclase activating polypeptide and **glucagon**-like peptide 1 and evidence against the existence of mammalian homologues.
AU Pohl, Markus; Wank, Stephen A. (1)
AB Helodermin and **exendin-4**, two peptides isolated from the salivary gland of the Gila monster, Heloderma suspectum, are approximately 50% homologous to vasoactive intestinal peptide (VIP) and **glucagon**-like peptide-1 (GLP-1), respectively, and interact with the mammalian receptors for VIP and GLP-1 with equal or higher affinity and efficacy. Immunohistochemical studies suggested the presence of helodermin-like peptides in mammals. To determine whether helodermin and **exendin-4** are present in mammals and their evolutionary

relationship to VIP and GLP-1, their cDNAs were first cloned from Gila monster salivary gland. Northern blots and reverse transcription-**polymerase** chain reaction of multiple Gila monster tissues identified apprx500-base pair transcripts only from salivary gland. Both helodermin and **exendin-4** full-length cDNAs were apprx500 base pairs long, and they encoded precursor proteins containing the entire amino acid sequence of helodermin and **exendin-4**, as well as a 44- or 45-amino acid N-terminal extension peptide, respectively, having apprx60% homology. The size and structural organization of these cDNAs indicated that they were closely related to one another but markedly different from known cDNAs for the VIP/GLP-1 peptide family previously identified in both lower and higher evolved species. Cloning of the Gila monster VIP/peptide histidine isoleucine, pituitary adenylate cyclase activating polypeptide, and **glucagon** / GLP-1 cDNAs and Southern blotting of Gila monster DNA demonstrate the coexistence of separate genes for these peptides and suggests, along with the restricted salivary gland expression, that helodermin and **exendin-4** coevolved to serve a separate specialized function. Probing of a variety of rat and human tissues on Northern blots, human and rat Southern blots, and genomic and cDNA libraries with either helodermin- or **exendin-4**-specific cDNAs failed to identify evidence for mammalian homologues. These data indicate that helodermin and **exendin-4** are not the precursors to VIP and GLP-1 and that they belong to a separate peptide family encoded by separate genes. Furthermore, the existence of as yet undiscovered mammalian homologues to helodermin and **exendin-4** seems unlikely.

ACCESSION NUMBER: 1998:222570 BIOSIS
DOCUMENT NUMBER: PREV199800222570
TITLE: Molecular cloning of the helodermin and **exendin-4** cDNAs in the lizard: Relationship to vasoactive intestinal polypeptide/pituitary adenylate cyclase activating polypeptide and **glucagon**-like peptide 1 and evidence against the existence of mammalian homologues.
AUTHOR(S): Pohl, Markus; Wank, Stephen A. (1)
CORPORATE SOURCE: (1) Build. 10, Room 9C-103, Natl. Inst. Health, Bethesda, MD 20892-1804 USA
SOURCE: Journal of Biological Chemistry, (April 17, 1998) Vol. 273, No. 16, pp. 9778-9784.
ISSN: 0021-9258.
DOCUMENT TYPE: Article
LANGUAGE: English

L249 ANSWER 8 OF 9 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 2
SO Journal of Biological Chemistry, (1997) Vol. 272, No. 7, pp. 4108-4115.
ISSN: 0021-9258.
TI Tissue-specific expression of unique mRNAs that encode proglucagon-derived peptides or exendin 4 in the lizard.
AU Chen, Yuqing E.; Drucker, Daniel J. (1)
AB **Glucagon**-like peptide 1 stimulates insulin secretion and inhibits **glucagon** secretion, gastric emptying, and feeding, suggesting it may be biologically useful for the treatment of diabetes. A lizard **glucagon**-like peptide 1 (GLP-1)-related peptide, **exendin 4**, binds to the GLP-1 receptor and mimics the actions of GLP-1 in vivo. To determine the genetic relationship between **exendin 4** and GLP-1, we analyzed the structure and expression of pancreatic and intestinal proglucagon mRNAs in the reptile Heloderma suspectum. Two different proglucagon cDNAs (lizard proglucagon I (LPI) and lizard proglucagon 11 (LPII)), with unique 3'-untranslated regions were identified. Two LPI mRNA transcripts, apprx 1.6 and 2.1 kilobases, encoded **glucagon** and GLP-1 but not GLP-2 and were restricted in expression to the pancreas. In contrast, a 1.1-kilobase LPII mRNA transcript, encoding **glucagon**, GLP-1, and GLP-2 utilized a different 3'-untranslated region and was expressed in both pancreas and

intestine. Lizard proglucagon mRNA transcripts were not detectable by reverse transcription-**polymerase** chain reaction or Northern blotting in salivary gland. A single class of lizard salivary gland proexendin cDNAs encoded the sequence of **exendin 4** and a 45-amino acid exendin NH-2-terminal peptide. Exendin mRNA transcripts were expressed in the salivary gland, but not pancreas or intestine. These data demonstrate that GLP-1 and **exendin 4** represent related yet distinct peptides encoded by different genes in the lizard.

ACCESSION NUMBER: 1997:126651 BIOSIS
DOCUMENT NUMBER: PREV199799418464
TITLE: Tissue-specific expression of unique mRNAs that encode proglucagon-derived peptides or exendin 4 in the lizard.
AUTHOR(S): Chen, Yuqing E.; Drucker, Daniel J. (1)
CORPORATE SOURCE: (1) Toronto Hosp., 200 Elizabeth St., CCRW3-838, Toronto, ON M5G 2C4 Canada
SOURCE: Journal of Biological Chemistry, (1997) Vol. 272, No. 7, pp. 4108-4115.
ISSN: 0021-9258.
DOCUMENT TYPE: Article
LANGUAGE: English

L249 ANSWER 9 OF 9 ADISINSIGHT COPYRIGHT (C) 2003 Adis Data Information BV
SO Adis R&D Insight

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=> s exendin-4 and (glucagonoma or necrolytic (w) migratory (w) erytherma)
L290          0 FILE DGENE
L291          0 FILE BIOSIS
L292          0 FILE SCISEARCH
L293          0 FILE EMBASE
L294          0 FILE ESBIOBASE
L295          1 FILE CAPLUS
L296          6 FILE USPATFULL
L297          0 FILE PASCAL
L298          0 FILE MEDLINE
L299          0 FILE DRUGU
L300          0 FILE BIOTECHNO
L301          0 FILE TOXCENTER
L302          0 FILE ADISCTI
L303          0 FILE LIFESCI
L304          2 FILE WPIDS
L305          0 FILE CANCERLIT
L306          0 FILE CIN
L307          0 FILE PROMT
L308          0 FILE CABA
L309          0 FILE NLDB
L310          0 FILE PHIN
L311          0 FILE ADISINSIGHT
L312          0 FILE EMBAL
L313          0 FILE BIOTECHDS
L314          0 FILE USPAT2
L315          0 FILE AGRICOLA
L316          1 FILE IFIPAT
L317          0 FILE JICST-EPLUS
L318          0 FILE PHARMAML
L319          0 FILE ADISNEWS
L320          0 FILE DRUGNL
L321          0 FILE IPA
L322          0 FILE AQUASCI
L323          0 FILE BIOCOMMERCE
L324          0 FILE DRUGUPDATES
L325          0 FILE FROSTI
L326          0 FILE FEDRIP
L327          0 FILE OCEAN
L328          0 FILE PHAR

TOTAL FOR ALL FILES
L329         10 EXENDIN-4 AND (GLUCAGONOMA OR NECROLYTIC (W) MIGRATORY (W) ERYTH
                ERMA)

=> dup rem l329
DUPLICATE IS NOT AVAILABLE IN 'DGENE, ADISINSIGHT, PHARMAML, ADISNEWS,
BIOCOMMERCE, DRUGUPDATES, FEDRIP, PHAR'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L329
L330          8 DUP REM L329 (2 DUPLICATES REMOVED)

=> d l330 1-8 ibib abs

L330 ANSWER 1 OF 8  USPATFULL                              DUPLICATE 1
ACCESSION NUMBER:       2003:4123  USPATFULL
TITLE:                  Use of glycogen phosphorylase inhibitors
INVENTOR(S):            Treadway, Judith L., Mystic, CT, UNITED STATES

                             NUMBER        KIND    DATE
                        ---------------- ------ --------
PATENT INFORMATION:     US 2003004162      A1   20030102
APPLICATION INFO.:      US 2001-813335     A1   20010320  (9)

                              NUMBER        DATE
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PRIORITY INFORMATION:	US 2000-191381P	20000322 (60)
DOCUMENT TYPE:	Utility	
FILE SEGMENT:	APPLICATION	
LEGAL REPRESENTATIVE:	Gregg C. Benson, Pfizer Inc., Patent Department, MS 4159,, Eastern Point Road, Groton, CT, 06340	
NUMBER OF CLAIMS:	23	
EXEMPLARY CLAIM:	1	
LINE COUNT:	4011	

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention provides methods of treating prophylactically an individual in whom Type 2 diabetes mellitus has not yet presented, but in whom there is an increased risk of developing such condition, which methods comprise administering to an individual in need thereof an effective amount of a glycogen phosphorylase inhibitor; effective amounts of a glycogen phosphorylase inhibitor and a non-glycogen phosphorylase inhibiting anti-diabetic agent; or effective amounts of a glycogen phosphorylase inhibitor and an anti-obesity agent.

The invention further provides methods of treating prophylactically an individual in whom Type 2 diabetes mellitus has not yet presented, but in whom there is an increased risk of developing such condition, which methods comprise administering to an individual in need thereof a pharmaceutical composition comprising effective amounts of a glycogen phosphorylase inhibitor and a non-glycogen phosphorylase inhibiting anti-diabetic agent; or effective amounts of a glycogen phosphorylase inhibitor and an anti-obesity agent.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L330 ANSWER 2 OF 8 USPATFULL

ACCESSION NUMBER:	2003:93670 USPATFULL		
TITLE:	Glucagon antagonists/inverse agonists		
INVENTOR(S):	Madsen, Peter, Bagsvaerd, DENMARK Lau, Jesper, Farum, DENMARK Ling, Anthony, San Diego, CA, UNITED STATES		

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2003065031	A1	20030403	
APPLICATION INFO.:	US 2001-996023	A1	20011116	(9)

	NUMBER	DATE
PRIORITY INFORMATION:	DK 2000-1731	20001117
	US 2000-252343P	20001120 (60)

DOCUMENT TYPE:	Utility
FILE SEGMENT:	APPLICATION
LEGAL REPRESENTATIVE:	Reza Green, Esq., Novo Nordisk of North America, Inc., Suite 6400, 405 Lexington Avenue, New York, NY, 10174-6401
NUMBER OF CLAIMS:	36
EXEMPLARY CLAIM:	1
LINE COUNT:	1907

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Novel compounds, which act to antagonize the action of the glucagon hormone on the glucagon receptor. Owing to their antagonizing effect of the glucagon receptor the compounds may be suitable for the treatment and/or prevention of any diseases and disorders, wherein a glucagon antagonistic action is beneficial, such as hyperglycemia, Type 1 diabetes, Type 2 diabetes, disorders of the lipid metabolism and obesity.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L330 ANSWER 3 OF 8 USPATFULL
ACCESSION NUMBER: 2003:38202 USPATFULL
TITLE: Glucagon antagonists/inverse agonists
INVENTOR(S): Jorgensen, Anker Steen, Kobenhavn O, DENMARK
Madsen, Peter, Bagsvaerd, DENMARK

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2003027849	A1	20030206
APPLICATION INFO.:	US 2001-995987	A1	20011116 (9)

	NUMBER	DATE
PRIORITY INFORMATION:	DK 2000-1733	20001117
	US 2000-252322P	20001120 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: Reza Green, Esq.,, Novo Nordisk of North America, Inc., Suite 6400, 405 Lexington Avenue, New York, NY, 10174-6401
NUMBER OF CLAIMS: 65
EXEMPLARY CLAIM: 1
LINE COUNT: 1902
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A novel class of compounds, which act to antagonize the action of the glucagon hormone on the glucagon receptor. Owing to their antagonizing effect of the glucagon receptor the compounds may be suitable for the treatment and/or prevention of any diseases and disorders, wherein a glucagon antagonistic action is beneficial, such as hyperglycemia, Type 1 diabetes, Type 2 diabetes, disorders of the lipid metabolism and obesity.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L330 ANSWER 4 OF 8 USPATFULL
ACCESSION NUMBER: 2003:60207 USPATFULL
TITLE: Peptide agonists of GLP-1 activity
INVENTOR(S): Larsen, Bjarne Due, Br.o slashed.nsh.o slashed.j, DENMARK
Mikkelsen, Jens Damsgaard, Lyngby, DENMARK
Neve, S.o slashed.ren, Lyngby, DENMARK
PATENT ASSIGNEE(S): Zealand Pharma A/S, Glostrup, DENMARK (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6528486	B1	20030304
APPLICATION INFO.:	US 2000-614847		20000712 (9)

	NUMBER	DATE
PRIORITY INFORMATION:	US 1999-143591P	19990712 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: Spector, Lorraine
ASSISTANT EXAMINER: Jiang, Dong
LEGAL REPRESENTATIVE: Buchanan, Robert L., Edwards & Angell, LLP
NUMBER OF CLAIMS: 2
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 8 Drawing Figure(s); 8 Drawing Page(s)
LINE COUNT: 3573
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to novel peptide conjugates which have increased stability and are useful in the treatment of excess levels of blood glucose.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L330 ANSWER 5 OF 8 USPATFULL
ACCESSION NUMBER: 2002:330297 USPATFULL
TITLE: Glucagon antagonists/inverse agonists
INVENTOR(S): Behrens, Carsten, Kobenhavn N, DENMARK
Lau, Jesper, Farum, DENMARK
Madsen, Peter, Bagsvaerd, DENMARK

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2002187982	A1	20021212
APPLICATION INFO.:	US 2001-996025	A1	20011116 (9)

	NUMBER	DATE
PRIORITY INFORMATION:	DK 2000-1732	20001117
	US 2000-252319P	20001120 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: Reza Green, Esq., Novo Nordisk of North America, Inc., 405 Lexington Avenue, Suite 6400, NewYork, NY, 10174-6401
NUMBER OF CLAIMS: 75
EXEMPLARY CLAIM: 1
LINE COUNT: 2710
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A novel class of compounds, which act to antagonize the action of the glucagon hormone on the glucagon receptor. Owing to their antagonizing effect of the glucagon receptor the compounds may be suitable for the treatment and/or prevention of any diseases and disorders, wherein a glucagon antagonistic action is beneficial, such as hyperglycemia, Type 1 diabetes, Type 2 diabetes, disorders of the lipid metabolism and obesity.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L330 ANSWER 6 OF 8 USPATFULL
ACCESSION NUMBER: 2002:259441 USPATFULL
TITLE: Treatment of diabetes mellitus
INVENTOR(S): Fryburg, David A., East Lyme, CT, UNITED STATES
Gibbs, Earl M., Oakdale, CT, UNITED STATES
Koppiker, Nandan P., Sandwich, UNITED KINGDOM

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2002143015	A1	20021003
APPLICATION INFO.:	US 2002-60788	A1	20020130 (10)

	NUMBER	DATE
PRIORITY INFORMATION:	GB 2001-6468	20010315
	US 2001-266083P	20010202 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: Gregg C. Benson, Pfizer Inc., Patent Department, MS 4159, Eastern Point Road, Groton, CT, 06340
NUMBER OF CLAIMS: 7
EXEMPLARY CLAIM: 1
LINE COUNT: 771
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Use of vardenafil or a pharmaceutical composition thereof in the preparation of a medicament for the curative, palliative or prophylactic treatment of type 2 diabetes mellitus.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L330 ANSWER 7 OF 8 WPIDS (C) 2003 THOMSON DERWENT
ACCESSION NUMBER: 2002-012518 [02] WPIDS
CROSS REFERENCE: 2000-595483 [50]; 2000-680964 [50]
DOC. NO. CPI: C2002-003289
TITLE: Use of glycogen phosphorylase inhibitor in prophylactic treatment of Type II diabetes.
DERWENT CLASS: B02
INVENTOR(S): TREADWAY, J L
PATENT ASSIGNEE(S): (PFIZ) PFIZER PROD INC; (TREA-I) TREADWAY J L
COUNTRY COUNT: 34
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
EP 1136071	A2	20010926	(200202)*	EN	78
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR					
AU 2001028130	A	20010927	(200202)		
CA 2341344	A1	20010922	(200203)	EN	
JP 2001302546	A	20011031	(200204)		70
HU 2001001158	A2	20020228	(200223)		
KR 2001092696	A	20011026	(200223)		
NZ 510677	A	20021025	(200274)		
US 2003004162	A1	20030102	(200305)		
ZA 2001002318	A	20021127	(200305)		154

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
EP 1136071	A2		EP 2001-301979	20010305
AU 2001028130	A		AU 2001-28130	20010320
CA 2341344	A1		CA 2001-2341344	20010320
JP 2001302546	A		JP 2001-78839	20010319
HU 2001001158	A2		HU 2001-1158	20010321
KR 2001092696	A		KR 2001-14306	20010320
NZ 510677	A		NZ 2001-510677	20010321
US 2003004162	A1	Provisional	US 2000-191381P	20000322
			US 2001-813335	20010320
ZA 2001002318	A		ZA 2001-2318	20010320

PRIORITY APPLN. INFO: US 2000-191381P 20000322; US 2001-813335 20010320
AN 2002-012518 [02] WPIDS
CR 2000-595483 [50]; 2000-680964 [50]
AB EP 1136071 A UPAB: 20020114
NOVELTY - A glycogen phosphorylase inhibitor (G1) is used in the manufacture of a medicament for prophylactically treating an individual with increased risk of developing Type II diabetes mellitus

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a pharmaceutical composition comprising (G1) and a non-glycogen phosphorylase inhibiting anti-diabetic agent (NG1); and

(2) a pharmaceutical composition comprising (G1) and an anti-obesity agent.

ACTIVITY - Antidiabetic.

MECHANISM OF ACTION - Glycogen phosphorylase inhibitor.

No biological data is given.

USE - For prophylactically treating a person having risk associated with Type 2 diabetes (particularly risk associated with insulin resistance and/or hyperinsulinemia; environmental or genetic Type 2 diabetes

predisposing disease states or conditions (e.g. person with a family history of diabetes); race and/or ethnicity (e.g. individuals from African-American, Hispanic, Native American, Asian, or Pacific Islander population); genetic mutations affecting beta -cell function (e.g. defect on chromosome 12, gene HNF-1 alpha (MODY3), chromosome 7, gene glucokinase (MODY2), chromosome 20, gene HNF-4a (MODY1), or mitochondrial DNA); genetic defects in insulin action (e.g. genetic mutation leading to Type A insulin resistance, acanthosis nigricans, leprechaunism, Rabson-Mendenhall syndrome, lipoatrophic diabetes, or a genetic mutation or mutations in the insulin receptor, IRS proteins, glucose transporters, PC-1, glucokinase, UCP-1, beta 3 adrenergic receptor gene); presence of excess adipose tissue or clinically diagnosed obesity (e.g. central obesity); clinical chemistry or diagnostic testing signifying a pre-diabetic state (e.g. impaired glucose tolerance, impaired fasting glucose, or hyperglycemia relative to normoglycemia); physiologic and endocrine changes associated with growth, development, or aging (e.g. menopausal, pubescent, or aged individuals); diet or eating behaviors (e.g consumption of high fat or high carbohydrate diets, experiencing prolonged fasting or starvation, having anorexia nervosa and bulemia); abnormal cardiovascular or blood lipid parameters (e.g. hypertension, HDL cholesterol level upto 35 mg/dl and/or TG levels of at least 250 mg/dl and metabolic syndrome); reproductive status (e.g. pregnancy, a history of gestational diabetes and macrosomia); muscle wasting (e.g. aging, starvation, exposure to anti-gravity environments and paralysis resulting from spinal cord injury); polycystic ovary syndrome; organ disease or dysfunction (e.g. liver cirrhosis and renal disease); metabolic disturbances; endocrine disorders or endocrinopathies (e.g. hyperandrogenism, thyrotoxicosis, hyperthyroidism, insulinoma, **glucagonoma**, somatostatinoma, aldosteroma, Cushing's Syndrome, pheochromocytoma, acromegaly and hypercortisolemia); pathophysiologic states (e.g. infection, congenital rubella, cytomegalovirus, toxemia, uremia, sepsis and trauma); immune-mediated disease (e.g. stiff man syndrome or the production of anti-insulin receptor antibodies); drug or chemical exposure (e.g. glucocorticoids, cytokines, alpha -interferon, thyroid hormone, TNF alpha , thiazides, estrogen-containing products, beta -blockers, nicotinic acid, serotonin receptor-targeted antipsychotics or antidepressants, vacor, diazoxide, dilantin, and HIV protease inhibitors); genetic syndrome associated with diabetes (e.g. Down's Syndrome, Klinefelter's Syndrome, Wolfram's Syndrome, Freidreich's Syndrome, Huntington's chorea, Laurence-Moon-Biedl Syndrome, myotonic dystrophy, porphyria, Prader-Willi Syndrome and Alzheimer's Disease); and detrimental effects caused by the administration of prolonged, elevated doses of insulin and/or the presence of ketoacidosis) (all claimed).
Dwg.0/0

L330 ANSWER 8 OF 8 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 2
ACCESSION NUMBER: 2000:493318 CAPLUS
DOCUMENT NUMBER: 133:129880
TITLE: Methods using an exendin or related substance for glucagon suppression
INVENTOR(S): Young, Andrew; Gedulin, Bronislava
PATENT ASSIGNEE(S): Amylin Pharmaceuticals, Inc., USA
SOURCE: PCT Int. Appl., 96 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 4
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000041548	A2	20000720	WO 2000-US942	20000114
WO 2000041548	A3	20001130		

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA,

MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI,
SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM,
AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE,
DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF,
CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

CA 2356331	AA	20000720	CA 2000-2356331	20000114
EP 1143989	A2	20011017	EP 2000-902415	20000114
EP 1143989	A3	20020911		

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
IE, SI, LT, LV, FI, RO

BR 2000007823	A	20011120	BR 2000-7823	20000114
JP 2002538084	T2	20021112	JP 2000-593169	20000114
NO 2001003469	A	20010914	NO 2001-3469	20010712

PRIORITY APPLN. INFO.:	US 1999-116380P	P	19990114
	US 1999-132017P	P	19990430
	US 2000-175365P	P	20000110
	WO 2000-US942	W	20000114

AB Methods are provided for use of an exendin, an exendin agonist, or a modified exendin or exendin agonist having an exendin or exendin agonist linked to one or more polyethylene glycol polymers, for example, for lowering glucagon levels and/or suppressing glucagon secretion in a subject. These methods are useful in treating hyperglucagonemia and other conditions that would be benefited by lowering plasma glucagon or suppressing glucagon secretion.

=>

[PDF]**EXENDIN**-4 (E4) AND **GLUCAGON**-LIKE PEPTIDE- 1 (GLP-1) IMPROVE ...
File Format: PDF/Adobe Acrobat - View as HTML
EXENDIN-4 (E4) AND **GLUCAGON**-LIKE PEPTIDE- 1 (GLP-1) IMPROVE GLUCOSE TOLERANCE AND
INDUCE ... saline), however, plasma insulin and **glucagon levels** remained unchanged ...
www.pancreasclub.com/PP2000-13.pdf - Similar pages

Exendin
... Ex-4 treated rats exhibited markedly reduced **levels** of fasting ... mass during the prediabetic
period with **glucagon**-like peptide-1 or **exendin**-4. Diabetes. ...
www.glucagon.com/exendin.htm - 19k - Jun 24, 2003 - Cached - Similar pages

Glucagon
... the GLP-1 receptor antagonist **exendin**(9-39 ... **Glucagon** generally functions as a counterregulatory
hormone, opposing ... of insulin, and maintaining the **levels** of blood ...
www.glucagon.com/glucagon.htm - 26k - Jun 24, 2003 - Cached - Similar pages
[More results from www.glucagon.com]

Amylin Product Pipeline - SYMLIN
... concentrations. Along with insulin, amylin concentrations normally
increase and **glucagon levels** decrease after meals. In people ...
www.amylin.com/website/Pipeline/Symlin.htm - 19k - Jun 24, 2003 - Cached - Similar pages

Amylin Product Pipeline - Exenatide
... Exenatide (synthetic **exendin**-4). ... have also shown that exenatide lowers post-meal **glucagon** concentrations and ... resulting in a marked reduction of HbA1c **levels**. ...
www.amylin.com/website/Pipeline/AC2993.htm - 16k - Jun 24, 2003 - Cached - Similar pages
[More results from www.amylin.com]

Effect of GIP and GLP-1 antagonists on insulin release in the rat ...
... meal-stimulated GLP-1 release was not affected by ANTGIP administration, whereas
postprandial **glucagon levels** were diminished in rats receiving **exendin**-(9-39 ...
www.ncbi.nlm.nih.gov/entrez/ query.fcgi?cmd=Retrieve&db=PubMed&list_uids=10362617&dopt=Abstract - Similar pages

Novel signal transduction and peptide specificity of **glucagon**- ...
... 1 such as GLP-2, GLP-1 (1-36), and **glucagon** all lowered cAMP **levels** in 3T3-L1 adipocytes.
In addition, an antagonist of pancreatic GLP-1 receptor, **exendin**-4 (9 ...
www.ncbi.nlm.nih.gov/entrez/ query.fcgi?cmd=Retrieve&db=PubMed&list_uids=97430848&dopt=Citation - Similar pages
[More results from www.ncbi.nlm.nih.gov]

Diabetes and Health News for 7/4/99: Couch potatoes twice as ...
... High **glucagon levels** are frequently found in both Type 1 and ... using agents like insulin, pramlintide, and **glucagon**-like peptide-1 [GLP-1]. **Exendin**-4 has ...
www.diabetesnet.com/news/news070499.php - 31k - Cached - Similar pages

Diabetes -- Abstracts: Scrocchi et al. 47 (4): 632
... for normal control of fasting and postabsorptive **glucagon levels**, and no ... During the Prediabetic Period With **Glucagon**-Like Peptide-1 or **Ex ndin**-4 Diabetes ...
diabetes.diabetesjournals.org/ cgi/content/abstract/47/4/632 - Similar pages

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Ode to a Gila Monster
... subcutaneous infusion of AC2993 (synthetic **exendin** 4) resulted in ... mL, and reduced plasma **glucagon** concentrations by ... decreases in blood glucose **levels** of nearly ...
www.medscape.com/viewarticle/442992_4 - 41k - Cached - Similar pages

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Medscape www.medscape.com
... fasting and daytime glucose **levels** in patients ... AC2993 (synthetic **exendin**-4) lowered
fasting glucose concentrations through suppression of **glucagon** and dose ...
www.medscape.com/viewarticle/442992_print - 23k - Cached - Similar pages
[More results,from www.medscape.com]

Diabetes for Professionals - Research Editorial - June 2003
... GLP-1 receptor agonist **exendin**-4 **Glucagon**-like peptide ... it was found that subcutaneously
administered **exendin**-4 lowered blood glucose **levels** in patients ...
www.d4pro.com/News/Items/ Research_Editorial_June_2003.asp - 25k - Cached - Similar pages

Diabetes In Control Dot Com.
... fasting, post-meal, and average blood sugar **levels**. ... and therapeutic potential of the **glucagon**-like peptides. ... **Exendin**-4 reduces fasting and postprandial glucose ...
www.diabetesincontrol.com/rosen/gilamonster.shtml - 29k - Cached - Similar pages

Could a GLP-I-based therapy ...
... in sham-operated control rats, rising to **levels** similar to ... increased number of extra-islet insulin (or **glucagon**)-positive cells in the **exendin**-4-treated ...
www.medforum.nl/idm/ could_a_glp-i-based_therapy____.htm - 18k - Cached - Similar pages

GLP-1 secretion is impaired in...
... AUC and in postprandial glucose **levels** in response ... **Glucagon**-like peptide 1 promotes satiety and suppresses ... DA, Habener JF, Bonner-Weir S. **Exendin**-4 stimulates b ...
www.medforum.nl/idm/ glp-1_secretion_is_impaired_in___.htm - 13k - Cached - Similar pages
[More results from www.medforum.nl]

Dia Care -- Abstracts: Toft-Nielsen et al. 22 (7): 1137
... of 1-mo bolus subcutaneous administration of **exendin**-4 in ... Legakis, C. Tzioras, and C. Phenekos Decreased **Glucagon**-Like Peptide 1 Fasting **Levels** in Type ...
care.diabetesjournals.org/cgi/ content/abstract/22/7/1137 - Similar pages

Diabetes -- Abstracts: Kolligs et al. 44 (1): 16
... D. Drucker, S. Efrat, and B. Thorens **Exendin**-(9-39 ... Is an Inverse Agonist of the Murine **Glucagon**-Like Peptide ... Cyclic Adenosine 3',5'-Monophosphate **Levels** and {beta ...
diabetes.diabetesjournals.org/ cgi/content/abstract/44/1/16 - Similar pages
[More results from diabetes.diabetesjournals.org]

Glucagon-like peptide 1 improved glycemic control in type 1 ...
... insulin treatment fail to achieve acceptable **levels** of hemoglobin ... JJ, & Rizza, RA: Effect of **glucagon**-like peptide ... Behme, MT, & McDonald, TJ: **Exendin**-4 reduces ...
www.pubmedcentral.nih.gov/ articlerender.fcgi?artid=154101 - Similar pages

BioMed Central | Full text | **Glucagon**-like peptide 1 improved ...
... insulin treatment fail to achieve acceptable **levels** of hemoglobin A1c ... JJ, Rizza RA: Effect of **glucagon**-like peptide-1 ... J, Behme MT, McDonald TJ: **Exendin**-4 reduces ...
www.biomedcentral.com/1472-6823/3/3 - 70k - Jun 24, 2003 - Cached - Similar pages

Lilly Newsroom - US Product News Releases
... Exenatide (synthetic **exendin**-4) is being studied for its ... insulin in response to elevated l **vels** of blood ... inhibition of the release of **glucagon** following meals ...

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newsroom.lilly.com/news/Product/ 2003-06-15_exenatide_type2diabetes.html - 22k - Jun 24, 2003 - Cached - Similar pages

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exendin and glucagon levels | Google Search | Search within results

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AGE annual meeting: submitted abstract

... **Glucagon** - like peptide - 1 (7-36) amide (GLP-1) may ... we now report that GLP-1 and **exendin**-4 exhibit anti ... GLP-1 dose-dependently reduces endogenous **levels** of A ...
www.americanaging.org/abs/Perry.htm - 4k - Cached - Similar pages

Search Results for **glucagon**

... from the liver causing blood glucose **levels** to rise ... **Glucagon** and Hypoglycemia new Proglucagon **glucagon** GLP-1 GLP-2 oxyntomodulin glicentin DP IV **Exendin**-4 GLP ...
eduforum.rug.ac.be/trefwoordenlink/ ENDO/files/GLUCAGON.HTM - 23k - Cached - Similar pages

Lilly and Amylin To Collaborate on Potential Breakthrough ...

... AC2993 decreases blood glucose toward normal **levels**. ... expected based on known **exendin**-4
actions ... insulin secretion, suppression of **glucagon** secretion, reduction ...
www.businesswire.com/webbox/bw.092002/222632055.htm - 12k - Cached - Similar pages

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[PDF]PII: S0014-5793(99)01112-6

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... h), Xenopus (xen) and gold¢sh (gf) **glucagon** and several ... hSEC), hPACAP-38, **exendin**-4 and **exendin** (9^39 ... cAMP **levels** are expressed as fold stimulation compared to ...
www.npb.ucdavis.edu/winter2003/128/ Ngan_et_al_FEBS_Letters_1999.pdf - Similar pages

Objectives

... hormone and reduces blood glucose **levels** by its ... stimulating insulin release, inhibition of **glucagon** secretion as ... identification of the compound **Exendin**-4. This ...
www.mydiabetologist.cc/English/ResearchInDiabetes/Contents/ EmergingDrugsToControlBloodSugarLevels.htm - 17k - Cached - Similar pages

Diabetes In Control Dot Com.

... glucose, and cholesterol **levels** down to acceptable **levels** even with ... genes, one of which encodes pro-**glucagon** and GLP-1, while the other encodes **exendin**-4. I ...
www.diabetesincontrol.com/rosen/battle.shtml - 28k - Cached - Similar pages
[More results from www.diabetesincontrol.com]

Biochemistry of Helodermatid Venom/Charles Eugene Lidikay

... This elicits no increase in cellular cAMP **levels** as it does not ... It is 48% homologous to human **glucagon** with the sequence ... **Exendin**-4 has also been described. ...
wwwchem.csustan.edu/chem4400/SJBR/venom.htm - 16k - Cached - Similar pages

Glucagon-like peptide-1 induces cell proliferation and pancreatic ...

... we show that continuous infusion of **glucagon**-like peptide ... The effects on **levels** of PDX-1 messenger RNA were abrogated by simultaneous infusion of **Exendin** (9-39 ...
www.arclab.org/medlineupdates/abstract_11108273.html - 6k - Cached - Similar pages

Target Diabetes - Novel approaches related to other pancreatic ...

... of interest is called GLP-1 (**glucagon**-like peptide ... shown that it reduces blood glucose **levels** after meals ... is also studying a compound (AC 2993, **Exendin**-4) which ...
www.abpi.org.uk/publications/publication_details/ targetDiabetes/section4e.asp - 28k - Cached - Similar pages

Type 1 News on the NDC Channel

... capable of making the hormones necessary for keeping people's blood-sugar l **vels** normal, Vinik ... The primary endpoint was **glucagon**-stimulated C-peptide production ...

Searched the web for **exendin and glucagon levels** . Results **41** - **50** of about **474**. Search took **0.17** seconds.

GLP and Receptor
... GLP-1 receptor antagonist, while **exendin** 4, is ... spanning receptors which include the **glucagon**, secretin, vasoactive ... These problems allow glucose **levels** to rise ...
www.igh.cnrs.fr/perso/cyril.sarrauste/job/glp/glp.html - 12k - Cached - Similar pages

Fiscal Year 2002 Director's Statement
... for increasing insulin demands; consequently, blood glucose **levels** rise ... GLP-1, a **glucagon**-like
gut peptide, can ... **Exendin**-4, a newly studied peptide analog of GLP ...
www.nia.nih.gov/about/legislation/fy2002/ds.htm - 20k - Cached - Similar pages

[PDF]New and Emerging Technology Briefing AC2993 for type 2 diabetes ...
File Format: PDF/Adobe Acrobat - View as HTML
... 2003 3 The technology AC2993 (synthetic **Exendin**-4/Exenatide ... with naturally occurring
human **glucagon**-like peptide ... deteriorates to unsatisfactory **levels** on current ...
www.publichealth.bham.ac.uk/horizon/ 2003%20reports/ac2993.pdf - Similar pages

[PDF]-Cell Differentiation from a Human Pancreatic Cell Line in Vitro ...
File Format: PDF/Adobe Acrobat - View as HTML
... cells, was expressed at high **levels** in lox5 ... aggregates, and lox5 treated with **exendin**-4.
A ... Insulin; B, other pancreatic hormones: PP, **glucagon**, somatostatin, and ...
icg.harvard.edu/~bio95hfj/assignments/ Dec17/dufayet_2001.pdf - Similar pages

[PDF]GLUCAGON-LIKE PEPTIDE-1 (TOTAL) RIA KIT 125 TUBES (Cat. # GLP1T- ...
File Format: PDF/Adobe Acrobat
... Extraction Procedure Note: Due to the low circulating **levels** of GLP ... 1 (7-37) (Human)
100 % GLP-2 (Human) < 0.01 % **Glucagon** (Human) 0.2 % **Exendin** < 0.01 % D ...
www.lincoresearch.com/protocols/pdf/glp1t-36hk.pdf - Similar pages

[PDF]BMC Endocrine Disorders
File Format: PDF/Adobe Acrobat - View as HTML
... insulin treatment fail to achieve acceptable **levels** of hemoglobin ... 365-367 Table 4:
Effects of **glucagon**-like peptide ... Behme MT and McDonald TJ **Exendin**-4 reduces ...
www.pubmedcentral.nih.gov/ picrender.fcgi?action=stream&blobtype=pdf&artid=154101 - Similar pages
[More results from www.pubmedcentral.nih.gov]

IMPACTING NEWS
... AC2993: This product is a synthetic **exendin**-4, whose actions ... Suppression of **glucagon** secretion ... of hypoglycemia (a fall of blood glucose to under normal **levels**.). ...
www.prohostonline.com/ImpactingNews/ impacting_news%20Amgen%20Amylin.htm - 33k - Cached - Similar pages

Type 2 News on the NDC Channel
... of complex, simultaneous changes in insulin and **glucagon levels** and possible effects on hepatic metabolism. Thus, the comparative effects of **exendin**-4 and GLP ...
www.diabetes-mellitus.org/news2.htm - 101k - Cached - Similar pages
[More results from www.diabetes-mellitus.org]

[PPT]Glucagon-like Peptide 1: Possible Therapy for Type 1 IDDM
File Format: Microsoft Powerpoint 97 - View as HTML
... However, with the introduction of **glucagon**-like peptide 1 (GLP-1 ... **Exendin** 9-39. ... It works through a Gs protein, therefore increasing intracellular cAMP **levels**. ...
socrates.barry.edu/snhs-plin/Endocrinology/Endo%20Presentations/ Mae%20De%20La%20Calzeda.ppt - Similar pages

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